



## SEQUENCE LISTING

<110> Watkins, Jeffrey D.  
Pancook, James D.

<120> Butyrylcholinesterase Variants That  
Alter the Activity of Chemotherapeutic Agents

<130> 66797-395

<140> US 10/728,723

<141> 2003-12-04

<150> US 10/310,666

<151> 2002-12-04

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Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser

50 55 60

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Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu

65 70 75 80

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85 90 95

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Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
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145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
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Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
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Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys	
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Phe	Ser	Lys	Asp 340	Asn	Asn	Ser	Ile	Ile 345	Thr	Arg	Lys	Glu	Phe	Gln	Glu 350
Gly	Leu	Lys 355	Ile	Phe	Phe	Pro	Gly 360	Val	Ser	Glu	Phe	Gly 365	Lys	Glu	Ser 370
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Tyr 385	Arg	Glu	Ala	Leu	Gly 390	Asp	Val	Val	Gly 395	Asp	Tyr	Asn	Phe	Ile	Cys 400
Pro	Ala	Leu	Glu	Phe 405	Thr	Lys	Lys	Phe	Ser 410	Glu	Trp	Gly	Asn	Asn	Ala 415
Phe	Phe	Tyr	Tyr 420	Phe	Glu	His	Arg	Ser 425	Ser	Lys	Leu	Pro	Trp 430	Pro	Glu 435
Trp	Met	Gly 435	Val	Met	His	Gly 440	Tyr	Glu	Ile	Glu	Phe 445	Val	Phe	Gly	Leu 450
Pro	Leu	Glu	Arg	Arg	Asp 455	Asn	Tyr	Thr	Lys	Ala	Glu 460	Glu	Ile	Leu	Ser 465
Arg 465	Ser	Ile	Val	Lys	Arg 470	Trp	Ala	Asn	Phe	Ala 475	Lys	Tyr	Gly	Asn	Pro 480
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Glu	Gln	Lys	Tyr 500	Leu	Thr	Leu	Asn	Thr 505	Glu	Ser	Thr	Arg	Ile	Met	Thr 510
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Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
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Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
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Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			
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Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
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Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
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Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205
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Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235
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Glu	Thr	Glu	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		260	265	270
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Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380
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Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415
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Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	515	520	525
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	530	535	540
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	545	550	555
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<223> synthetic butyrylcholinesterase variant

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Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576



Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
		210					215				220					
ggc	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggc	tgc	tct	aga	gag	aat	768
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245						250					255	
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	cag	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Gln	Ser	Val	
		275					280					285				
aac	ttt	ggc	ccg	acc	gtg	gat	ggc	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggc	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggc	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325				330					335			
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggc	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggc	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390				395						400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	

405	410	415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495			1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510			1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525			1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540			1632
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln 545 550 555 560			1680
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu 565 570			1722

&lt;210&gt; 6

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 6

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Gln	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365	
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395	400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430	
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445	
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser				

450	455	460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro		
465	470	475
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr		
	485	490
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr		495
	500	505
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys		510
	515	520
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys		525
	530	535
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln		540
545	550	555
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu		560
	565	570

&lt;210&gt; 7

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 7

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384

Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct tgc tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Ser Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	

340	345	350	
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495			1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510			1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525			1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540			1632
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln 545 550 555 560			1680
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu 565 570			1722

<210> 8  
 <211> 574  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic butyrylcholinesterase variant

<220>  
 <221>VARIANT  
 <222> 227

<223> Xaa = Ala

<400> 8  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Ser Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly

				325					330					335		
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
	450					455					460					
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490					495		
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
			500					505					510			
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	
	530					535					540					
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	
545					550					555					560	
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu			
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<210> 9
<211> 1722
<212> DNA
<213> Artificial Sequence
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<220>  
<221> CDS  
<222> (1)...(1722)
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<223> synthetic butyrylcholinesterase variant

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Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met																	
1		5					10					15					
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc																	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro																	
		20					25					30					
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct																	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser																	
		35					40					45					
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat qca aat tct																	192



Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
50						55					60					
tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65					70					75					80	
atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		
gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			
att	tat	ggg	ggg	ggg	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				
gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					
aac	tat	agg	gtg	ggg	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	
gag	gct	cca	ggg	aac	atg	ggg	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
			165						170					175		
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggg	gga	aat	cct	aaa	agt	gta	576
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
		210					215				220					
ggg	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggg	tgc	tct	aga	gag	aat	768
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
			245						250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	cat	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	His	Ser	Val	

275	280	285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495			1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510			1536

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
           515                               520                               525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
           530                               535                               540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
           545                               550                               555                               560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
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<213> Artificial Sequence

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<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

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           20                  25                  30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
           35                  40                  45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
           50                  55                  60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
   65                  70                  75                  80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
           85                  90                  95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
           100                  105                  110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
           115                  120                  125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
           130                  135                  140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
   145                  150                  155                  160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
           165                  170                  175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
           180                  185                  190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
           195                  200                  205

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Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg
225                230                235                240
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn
                245                250                255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile
                260                265                270
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro His Ser Val
                275                280                285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp
                290                295                300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly
305                310                315                320
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly
                325                330                335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
                340                345                350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
                355                360                365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
370                375                380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385                390                395                400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
                405                410                415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
                420                425                430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
                435                440                445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
450                455                460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465                470                475                480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
                485                490                495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
500                505                510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
515                520                525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
530                535                540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545                550                555                560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
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<210> 11

<211> 1722

<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	

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Gly Ser Ala Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct tgg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Trp Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	

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Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
450 455 460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545 550 555 560

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<210> 12

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<400> 12

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Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
35 40 45
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
50 55 60
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu
65 70 75 80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn
85 90 95
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp
100 105 110
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr

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115	120	125
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Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln		
165	170	175
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val		
180	185	190
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu		
195	200	205
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser		
210	215	220
Gly Ser Ala Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg		
225	230	235
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn		
245	250	255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile		
260	265	270
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Trp Ser Val		
275	280	285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp		
290	295	300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly		
305	310	315
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly		
325	330	335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu		
340	345	350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser		
355	360	365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn		
370	375	380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys		
385	390	395
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala		
405	410	415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu		
420	425	430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu		
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Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser		
450	455	460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro		
465	470	475
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr		
485	490	495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr		
500	505	510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys		
515	520	525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys		
530	535	540
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<210> 13  
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 <222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 13

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Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag'cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	

tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggg tcc gcg aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Ala Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg cck gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Xaa Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	

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cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc      1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
      405                      410                      415

ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa      1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
      420                      425                      430

tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta      1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
      435                      440                      445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt      1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
      450                      455                      460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca      1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
      465                      470                      475                      480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act      1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
      485                      490                      495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg      1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
      500                      505                      510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa      1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
      515                      520                      525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa      1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
      530                      535                      540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa      1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
      545                      550                      555                      560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc      1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
      565                      570

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<210> 14

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 287

&lt;223&gt; Xaa = Pro

&lt;400&gt; 14

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
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Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
	195						200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Ala	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225					230					235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Xaa	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400

Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 15

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 15

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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn

																85																	90																	95																
gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336																																																		
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp																																																			
			100							105							110																																																	
att	tat	ggg	ggg	ggg	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384																																																		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr																																																			
			115							120							125																																																	
gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432																																																		
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met																																																			
			130							135							140																																																	
aac	tat	agg	gtg	ggg	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480																																																		
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro																																																			
			145							150							155																																																	
gag	gct	cca	ggg	aac	atg	ggg	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528																																																		
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln																																																			
			165							170							175																																																	
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggg	gga	aat	cct	aaa	agt	gta	576																																																		
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val																																																			
			180							185							190																																																	
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624																																																		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu																																																			
			195							200							205																																																	
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672																																																		
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser																																																			
			210							215							220																																																	
ggg	tcc	gcg	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720																																																		
Gly	Ser	Ala	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg																																																			
			225							230							235																																																	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggg	tgc	tct	aga	gag	aat	768																																																		
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn																																																			
			245							250							255																																																	
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816																																																		
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile																																																			
			260							265							270																																																	
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	ggg	gta	864																																																		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Gly	Val																																																			
			275							280							285																																																	
aac	ttt	ggg																																																																

gtt aat aaa gat gaa ggg aca tgg ttt tta gtc atg ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Trp Phe Leu Val Met Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465 470 475 480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act	1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr	
485 490 495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg	1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr	
500 505 510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa	1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys	
515 520 525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa	1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys	
530 535 540	

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 16

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<400> 16

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 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Ala Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Gly Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly



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305          310          315          320
Val Asn Lys Asp Glu Gly Thr Trp Phe Leu Val Met Gly Ala Pro Gly
          325          330          335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
          340          345          350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
          355          360          365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
          370          375          380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385          390          395          400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
          405          410          415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
          420          425          430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
          435          440          445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
          450          455          460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465          470          475          480
Asn Glu Thr Gln Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
          485          490          495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
          500          505          510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
          515          520          525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
          530          535          540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545          550          555          560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
          565          570

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<210> 17

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(711)

<223> synthetic butyrylcholinesterase variant

<400> 17

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atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg      48
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
  1              5              10              15

ctc cca ggt gcc aaa tgt gac atc ttg ctg act cag tct cca gtc atc      96
Leu Pro Gly Ala Lys Cys Asp Ile Leu Leu Thr Gln Ser Pro Val Ile
          20              25              30

ctg tct gtg agt cca gga gaa aga gtc agt ttc tcc tgc agg gcc agt      144
Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys Arg Ala Ser

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35	40	45	
cag agt att ggc aca aac ata cac tgg tat cag caa aga aca aat ggt Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg Thr Asn Gly 50 55 60			192
tct cca agg ctt ctc ata aag tat gct tct gag tct atc tct ggg atc Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile 65 70 75 80			240
cct tcc agg ttt agt ggc agt gga tca ggg aca gat ttt act ctt agc Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser 85 90 95			288
atc aac agt gtg gag tct gaa gat att gca gat tat tac tgt caa caa Ile Asn Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln 100 105 110			336
aat aat aac tgg cca acc acg ttc ggt gct ggg acc aag ctg gag ctg Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu 115 120 125			384
aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp 130 135 140			432
gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn 145 150 155 160			480
ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu 165 170 175			528
caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp 180 185 190			576
agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr 195 200 205			624
gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser 210 215 220			672
tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys * 225 230 235			711

&lt;210&gt; 18

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 18

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Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1          5          10          15
Leu Pro Gly Ala Lys Cys Asp Ile Leu Leu Thr Gln Ser Pro Val Ile
 20          25          30
Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys Arg Ala Ser
 35          40          45
Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg Thr Asn Gly
 50          55          60
Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile
 65          70          75          80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser
 85          90          95
Ile Asn Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln
100          105          110
Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
115          120          125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130          135          140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145          150          155          160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165          170          175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180          185          190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195          200          205
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
210          215          220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225          230          235

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&lt;210&gt; 19

&lt;211&gt; 2349

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(2349)

&lt;400&gt; 19

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atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt      48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1          5          10          15

gtc cac tcc cag gtg cag ctg aag cag tca gga cct ggc cta gtg cag      96
Val His Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln
 20          25          30

ccc tca cag agc ctg tcc atc acc tgc aca gtc tct ggt ttc tca tta      144
Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
 35          40          45

act aac tat ggt gta cac tgg gtt cgc cag tct cca gga aag ggt ctg      192

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Thr	Asn	Tyr	Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	
50						55					60					
gag	tgg	ctg	gga	gtg	ata	tgg	agt	ggt	gga	aac	aca	gac	tat	aat	aca	240
Glu	Trp	Leu	Gly	Val	Ile	Trp	Ser	Gly	Gly	Asn	Thr	Asp	Tyr	Asn	Thr	
65					70					75					80	
cct	ttc	aca	tcc	aga	ctg	agc	atc	aac	aag	gac	aat	tcc	aag	agc	caa	288
Pro	Phe	Thr	Ser	Arg	Leu	Ser	Ile	Asn	Lys	Asp	Asn	Ser	Lys	Ser	Gln	
				85					90					95		
gtt	ttc	ttt	aaa	atg	aac	agt	ctg	caa	tct	aat	gac	aca	gcc	ata	tat	336
Val	Phe	Phe	Lys	Met	Asn	Ser	Leu	Gln	Ser	Asn	Asp	Thr	Ala	Ile	Tyr	
			100					105					110			
tac	tgt	gcc	aga	gcc	ctc	acc	tac	tat	gat	tac	gag	ttt	gct	tac	tgg	384
Tyr	Cys	Ala	Arg	Ala	Leu	Thr	Tyr	Tyr	Asp	Tyr	Glu	Phe	Ala	Tyr	Trp	
		115					120					125				
ggc	caa	ggg	act	ctg	gtc	act	gtc	tct	gca	gcc	tcc	acc	aag	ggc	cca	432
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Ala	Ser	Thr	Lys	Gly	Pro	
	130					135					140					
tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	480
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	
145					150					155					160	
gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	528
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	
				165					170					175		
gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	576
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	
			180					185					190			
gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	624
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	
		195					200					205				
gtg	ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	672
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	
	210					215					220					
cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gca	gag	ccc	aaa	tct	720
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	
225					230					235					240	
tgt	gac	aaa	act	cac	aca	tgt	cca	ccg	tgt	cca	aag	ctt	gaa	gat	gac	768
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Lys	Leu	Glu	Asp	Asp	
				245					250					255		
atc	ata	att	gca	aca	aag	aat	gga	aaa	gtc	aga	ggg	atg	aac	ttg	aca	816
Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	Asn	Leu	Thr	
			260					265					270			
gtt	ttt	ggt	ggc	acg	gta	aca	gcc	ttt	ctt	gga	att	ccc	tat	gca	cag	864
Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	Tyr	Ala	Gln	

275	280	285	
cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct ctg acc aag Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys 290 295 300			912
tgg tct gat att tgg aat gcc aca aaa tat gca aat tct tgc tgt cag Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser Cys Cys Gln 305 310 315 320			960
aac ata gat caa agt ttt cca ggc ttc cat gga tca gag atg tgg aac Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu Met Trp Asn 325 330 335			1008
cca aac act gac ctc agt gaa gac tgt tta tat cta aat gta tgg att Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ile 340 345 350			1056
cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg att tat ggt Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp Ile Tyr Gly 355 360 365			1104
ggg ggt ttt caa act gga aca tca tct tta cat gtt tat gat ggc aag Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr Asp Gly Lys 370 375 380			1152
ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg aac tat agg Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met Asn Tyr Arg 385 390 395 400			1200
gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct gag gct cca Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro Glu Ala Pro 405 410 415			1248
ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag tgg gtt caa Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln Trp Val Gln 420 425 430			1296
aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta act ctc ttt Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val Thr Leu Phe 435 440 445			1344
gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg ctt tct cct Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu Leu Ser Pro 450 455 460			1392
gga agc cat tca ttg ttc acc aga gcc att ctg caa agt ggt tcc ttt Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser Gly Ser Phe 465 470 475 480			1440
aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg aac aga acg Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg Asn Arg Thr 485 490 495			1488
ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat gag act gaa Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn Glu Thr Glu 500 505 510			1536

ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att ctt ctg aat Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile Leu Leu Asn 515 520 525	1584
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ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac ata tta ctt Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp Ile Leu Leu 545 550 555 560	1680
gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt gtt aat aaa Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly Val Asn Lys 565 570 575	1728
gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc ttc agc aaa Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys 580 585 590	1776
gat aac aat agt atc ata act aga aaa gaa ttt cag gaa ggt tta aaa Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu Gly Leu Lys 595 600 605	1824
ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc atc ctt ttt Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser Ile Leu Phe 610 615 620	1872
cat tac aca gac tgg gta gat gat cag aga cct gaa aac tac cgt gag His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr Arg Glu 625 630 635 640	1920
gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc cct gcc ttg Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys Pro Ala Leu 645 650 655	1968
gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc ttt ttc tac Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr 660 665 670	2016
tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa tgg atg gga Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met Gly 675 680 685	2064
gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta cct ctg gaa Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu Glu 690 695 700	2112
aga aga gat aat tac aca aaa gcc gag gaa att ttg agt aga tcc ata Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile 705 710 715 720	2160
gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca aat gag act Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn Glu Thr 725 730 735	2208

cag aac aat agc aca agc tgg cct gtc ttc aaa agc act gaa caa aaa 2256  
 Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys  
                   740                                  745                                  750

tat cta acc ttg aat aca gag tca aca aga ata atg acg aaa cta cgt 2304  
 Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr Lys Leu Arg  
                   755                                  760                                  765

gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa gtc tga 2349  
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<210> 20

<211> 782

<212> PRT

<213> Mus musculus

<400> 20

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                   20                                  25                                  30  
 Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu  
                   35                                  40                                  45  
 Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu  
                   50                                  55                                  60  
 Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr  
 65                                  70                                  75                                  80  
 Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln  
                                   85                                  90                                  95  
 Val Phe Phe Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr  
                   100                                  105                                  110  
 Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp  
                   115                                  120                                  125  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro  
 130                                  135                                  140  
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr  
 145                                  150                                  155                                  160  
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr  
                   165                                  170                                  175  
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro  
                   180                                  185                                  190  
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
                   195                                  200                                  205  
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn  
 210                                  215                                  220  
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser  
 225                                  230                                  235                                  240  
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Lys Leu Glu Asp Asp  
                   245                                  250                                  255  
 Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met Asn Leu Thr  
                   260                                  265                                  270  
 Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro Tyr Ala Gln  
                   275                                  280                                  285  
 Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys  
 290                                  295                                  300  
 Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser Cys Cys Gln

305					310					315				320
Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	Met	Trp
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Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp
			340					345					350	
Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	Ile	Tyr
		355					360					365		
Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	Asp	Gly
	370					375					380			
Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	Asn	Tyr
385					390				395					400
Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	Glu	Ala
				405				410						415
Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	Trp	Val
			420					425					430	
Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	Thr	Leu
	435						440					445		
Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	Leu	Ser
	450					455					460			
Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	Gly	Ser
465					470					475				480
Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	Asn	Arg
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Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	Glu	Thr
			500					505					510	
Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	Leu	Leu
	515						520					525		
Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	Asn	Phe
	530					535					540			
Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	Ile	Leu
545					550					555				560
Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	Val	Asn
			565					570						575
Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	Phe	Ser
			580					585					590	
Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	Gly	Leu
	595						600					605		
Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	Ile	Leu
	610					615					620			
His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	Tyr	Arg
625					630					635				640
Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	Pro	Ala
			645					650					655	
Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	Phe	Phe
		660						665					670	
Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	Trp	Met
	675						680					685		
Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	Pro	Leu
	690					695					700			
Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	Arg	Ser
705					710					715				720
Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	Asn	Glu
			725						730					735
Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	Glu	Gln
			740					745					750	
Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	Lys	Leu
	755						760							



Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys Val  
 770 775 780

<210> 21

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 21

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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat 384  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg 432  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct 480  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag 528  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln

165						170						175						
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggt	gga	aat	cct	aaa	agt	gta	576		
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val			
		180						185					190					
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu			
		195					200					205						
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672		
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser			
		210				215					220							
ggt	tcc	ttt	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720		
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg			
225					230					235					240			
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggt	tgc	tct	aga	gag	aat	768		
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn			
				245					250					255				
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816		
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile			
			260					265					270					
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val			
		275					280					285						
aac	ttt	ggt	ccg	acc	gtg	gat	ggt	gat	ttt	ctc	act	gac	atg	cca	gac	912		
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp			
	290					295					300							
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960		
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly			
305					310					315					320			
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008		
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly			
				325				330					335					
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056		
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu			
			340					345					350					
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser			
		355					360					365						
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152		
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn			
		370				375												

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cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc 1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
      405                      410                      415

ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa 1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
      420                      425                      430

tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta 1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
      435                      440                      445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
      450                      455                      460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
      465                      470                      475                      480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
      485                      490                      495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
      500                      505                      510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
      515                      520                      525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
      530                      535                      540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
      545                      550                      555                      560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
      565                      570

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&lt;210&gt; 22

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 22

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Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met
1           5           10           15

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Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	450	455	460
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro			

465		470		475		480
Asn Glu Thr Gln	Asn Asn Ser Thr Ser Trp	Pro Val Phe Lys Ser Thr				
	485	490		495		
Glu Gln Lys Tyr	Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr					
	500	505		510		
Lys Leu Arg Ala	Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys					
	515	520		525		
Val Leu Glu Met Thr	Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys					
	530	535		540		
Ala Gly Phe His Arg	Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln					
	545	550		555		560
Phe Asn Asp Tyr Thr	Ser Lys Lys Glu Ser Cys Val Gly Leu					
	565	570				

&lt;210&gt; 23

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 23

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aag ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Lys Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056

ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510	1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525	1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540	1632
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln 545 550 555 560	1680
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu 565 570	1722

<211> 574  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic butyrylcholinesterase variant

<220>  
 <221> VARIANT  
 <222> 227  
 <223> Xaa = Ala

<400> 24  
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 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Lys Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly  
 325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350



Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 25

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 25

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 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag cgg ata gat caa agt ttt cca ggc ttc cat gga tca gag Cys Cys Gln Arg Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu 65 70 75 80	240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95	288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110	336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125	384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912

Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggc tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510	1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys	1584

515	520	525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa			1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys			
530	535	540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa			1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln			
545	550	555	560
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc			1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu			
565	570		

&lt;210&gt; 26

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 26

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met			
1	5	10	15
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro			
20	25	30	
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser			
35	40	45	
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser			
50	55	60	
Cys Cys Gln Arg Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu			
65	70	75	80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn			
85	90	95	
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp			
100	105	110	
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr			
115	120	125	
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met			
130	135	140	
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro			
145	150	155	160
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln			
165	170	175	
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val			
180	185	190	
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu			
195	200	205	
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser			
210	215	220	

Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365	
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395	400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430	
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445	
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	450	455	460	
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	465	470	475	480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	485	490	495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	500	505	510	
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	515	520	525	
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	530	535	540	
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	545	550	555	560
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu			565	570		

&lt;210&gt; 27

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 27

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met 1 5 10 15	48
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro 20 25 30	96
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser 35 40 45	144
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser 50 55 60	192
tgc tgt cag aac ata ggg caa agt ttt cca ggc ttc cat gga tca gag Cys Cys Gln Asn Ile Gly Gln Ser Phe Pro Gly Phe His Gly Ser Glu 65 70 75 80	240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95	288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110	336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125	384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720

Gly 225	Ser	Xaa	Asn	Ala	Pro 230	Trp	Ala	Val	Thr	Ser 235	Leu	Tyr	Glu	Ala	Arg 240	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggg	tgc	tct	aga	gag	aat	768
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
			245						250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
aac	ttt	ggg	ccg	acc	gtg	gat	ggg	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggg	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggg	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
			325						330				335			
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggg	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggg	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggg	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	

450	455	460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca			1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro			
465	470	475	480
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act			1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr			
485	490	495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg			1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr			
500	505	510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa			1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys			
515	520	525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa			1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys			
530	535	540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa			1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln			
545	550	555	560
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc			1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu			
565	570		

&lt;210&gt; 28

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 28

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met			
1	5	10	15
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro			
20	25	30	
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser			
35	40	45	
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser			
50	55	60	
Cys Cys Gln Asn Ile Gly Gln Ser Phe Pro Gly Phe His Gly Ser Glu			
65	70	75	80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn			
85	90	95	



Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	450	455	460
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	465	470	475
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	485	490	495
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	500	505	510
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	515	520	525
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	530	535	540
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln			

<210> 29  
<211> 1722  
<212> DNA

```
<220>  
<221> CDS  
<222> (1)...(1722)
```

<400> 29																	
gaa	gat	gac	atc	ata	att	gca	aca	aag	aat	gga	aaa	gtc	aga	ggg	atg	48	
Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met		
1				5					10					15			
aac	ttg	aca	gtt	ttt	ggg	ggc	acg	gta	aca	gcc	ttt	ctt	gga	att	ccc	96	
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro		
			20					25					30				
tat	gca	cag	cca	cct	ctt	ggg	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser		
		35					40					45					
ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser		
	50					55					60						
tgc	tgt	cag	aac	ata	cat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240	
Cys	Cys	Gln	Asn	Ile	His	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu		
65				70						75				80			
atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288	
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn		
				85					90					95			
gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp		
			100					105					110				
att	tat	ggg	ggg	ggg	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		
		115					120					125					
gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met		
	130					135					140						
aac	tat	agg	gtg	ggg	ggc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro		
145				150						155					160		

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tggt gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggg tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	

tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465 470 475 480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act	1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr	
485 490 495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg	1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr	
500 505 510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa	1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys	
515 520 525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa	1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys	
530 535 540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa	1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln	
545 550 555 560	
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc	1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu	
565 570	

&lt;210&gt; 30

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 30

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
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Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	His	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65				70					75						80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
			85					90					95		
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120						125		
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145				150					155						160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165				170					175		
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
	195						200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230						235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
			245					250					255		
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
		260					265					270			
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
			325					330					335		
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340				345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385				390						395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala

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                405                410                415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
                420                425                430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
                435                440                445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
                450                455                460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465                470                475                480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
                485                490                495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
                500                505                510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
                515                520                525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
                530                535                540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545                550                555                560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
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<210> 31

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 31

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 1                5                10                15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc      96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
                20                25                30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct     144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
                35                40                45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct     192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
                50                55                60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc ttc gga tca gag     240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe Phe Gly Ser Glu
        65                70                75                80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat     288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn

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85	90	95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110			336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125			384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140			432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160			480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175			528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190			576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205			624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960

gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggc tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510	1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525	1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540	1632



gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 32

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 32

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 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe Phe Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270

Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly  
 325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350  
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
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<210> 33

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 33

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 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96

Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro		
			20					25					30				
tat	gca	cag	cca	cct	ctt	ggc	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser		
		35					40					45					
ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser		
		50				55					60						
tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cct	gga	tca	gag	240	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	Pro	Gly	Ser	Glu		
	65					70				75					80		
atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288	
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn		
				85					90					95			
gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp		
			100					105					110				
att	tat	ggc	ggc	ggc	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		
		115					120					125					
gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met		
	130					135					140						
aac	tat	agg	gtg	ggc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct		480	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro		
	145				150				155					160			
gag	gct	cca	ggg	aac	atg	ggc	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln		
			165						170					175			
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggc	gga	aat	cct	aaa	agt	gta	576	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val		
			180					185					190				
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195					200					205					
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
		210					215				220						
ggc	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
	225				230					235				240			
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggc	tgc	tct	aga	gag	aat	768	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		

245	250	255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggc tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
                   485                  490                  495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                   500                  505                  510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
                   515                  520                  525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
                   530                  535                  540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
                   545                  550                  555                  560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                   565                  570

<210> 34

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 34

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1                  5                  10                  15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
                   20                  25                  30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
                   35                  40                  45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
                   50                  55                  60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe Pro Gly Ser Glu  
 65                  70                  75                  80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
                   85                  90                  95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
                   100                  105                  110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
                   115                  120                  125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met

<210> 35

<211> 1722  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 35

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	

att tat ggt ggt ggt ttt caa tgg gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Trp Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	

tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	

180	185	190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205			624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248



ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa 1296  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430

tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta 1344  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 36

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 36

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Trp	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255
Glu	Thr	Glu	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		260	265	270
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	450	455	460
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro			

465		470		475		480
Asn Glu Thr Gln	Asn Asn Ser Thr Ser Trp	Pro Val Phe Lys Ser Thr				
	485	490		495		
Glu Gln Lys Tyr	Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr					
	500	505		510		
Lys Leu Arg Ala	Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys					
	515	520		525		
Val Leu Glu Met	Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys					
	530	535		540		
Ala Gly Phe His	Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln					
	545	550		555		560
Phe Asn Asp Tyr	Thr Ser Lys Lys Glu Ser Cys Val Gly Leu					
	565	570				

&lt;210&gt; 37

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 37

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa tat gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Tyr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056

ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510	1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525	1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540	1632
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln 545 550 555 560	1680
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu 565 570	1722

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 38

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Tyr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350	

Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
           355                                  360                  365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
           370                                  375                  380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385                                  390                  395                  400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
                                   405                                  410                  415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
                                   420                                  425                  430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
                                   435                                  440                  445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
                                   450                                  455                  460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465                                  470                  475                  480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
                                   485                                  490                  495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                                   500                                  505                  510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
                                   515                                  520                  525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
                                   530                                  535                  540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545                                  550                  555                  560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                                   565                                  570

<210> 39

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 39

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met

1

5

10

15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96

Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro

20

25

30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144

Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser

35

40

45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192

Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser

50

55

60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu 65 70 75 80	240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95	288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110	336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125	384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc ggt ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Gly Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912



Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
290						295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
ggt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	ggt	ggt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
		450				455					460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490					495		
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
			500					505					510			
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	

515	520	525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa			1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys			
530	535	540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa			1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln			
545	550	555	560
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc			1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu			
565	570		

&lt;210&gt; 40

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 40

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met			
1	5	10	15
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro			
20	25	30	
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser			
35	40	45	
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser			
50	55	60	
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu			
65	70	75	80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn			
85	90	95	
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp			
100	105	110	
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr			
115	120	125	
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met			
130	135	140	
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro			
145	150	155	160
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln			
165	170	175	
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val			
180	185	190	
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu			
195	200	205	
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser			
210	215	220	
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg			

225		230		235		240
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn						
	245			250		255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile						
	260			265		270
Leu Leu Asn Glu Ala Phe Val Val Pro Gly Gly Thr Pro Leu Ser Val						
	275			280		285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp						
	290			295		300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly						
305		310		315		320
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly						
	325			330		335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu						
	340			345		350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser						
	355			360		365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn						
370		375		380		
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys						
385		390		395		400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala						
	405			410		415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu						
	420			425		430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu						
	435			440		445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser						
	450			455		460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro						
465		470		475		480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr						
	485			490		495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr						
	500			505		510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys						
	515			520		525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys						
	530			535		540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln						
545		550		555		560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu						
	565			570		

&lt;210&gt; 41

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 41

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg

48

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	
1				5					10					15		
aac	ttg	aca	gtt	ttt	ggt	ggc	acg	gta	aca	gcc	ttt	ctt	gga	att	ccc	96
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	
			20					25					30			
tat	gca	cag	cca	cct	ctt	ggt	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
			35				40					45				
ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50					55					60					
tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65					70					75					80	
atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
			85						90					95		
gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			
att	tat	ggt	ggt	ggt	ttt	caa	act	gga	aca	tca	tct	tta	cat	ggt	tat	384
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115				120						125				
gat	ggc	aag	ttt	ctg	gct	cgg	ggt	gaa	aga	ggt	att	gta	gtg	tca	atg	432
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135				140						
aac	tat	agg	gtg	ggt	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145				150						155					160	
gag	gct	cca	ggg	aac	atg	ggt	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
			165						170				175			
tgg	ggt	caa	aaa	aat	ata	gca	gcc	ttt	ggt	gga	aat	cct	aaa	agt	gta	576
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	ggt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195				200						205				
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
	210					215					220					
ggt	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720

Gly 225	Ser	Xaa	Asn	Ala	Pro 230	Trp	Ala	Val	Thr	Ser 235	Leu	Tyr	Glu	Ala	Arg 240	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggg	tgc	tct	aga	gag	aat	768
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
			245						250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	aat	ggg	act	cct	ttg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Asn	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
aac	ttt	ggg	ccg	acc	gtg	gat	ggg	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggg	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggg	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggg	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggg	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggg	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	

450	455	460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca			1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro			
465	470	475	480
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act			1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr			
485	490		495
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg			1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr			
500	505		510
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa			1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys			
515	520		525
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa			1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys			
530	535		540
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa			1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln			
545	550		555
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc			1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu			
565	570		

&lt;210&gt; 42

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 42

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met			
1	5	10	15
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro			
20	25		30
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser			
35	40		45
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser			
50	55		60
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu			
65	70		75
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn			
85	90		95
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp			

Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
		130				135					140					
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
				165					170						175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185				190				
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
		210				215					220					
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245						250				255		
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Asn	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
		290				295					300					
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325						330				335		
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405						410				415		
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440									

Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 43

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 43

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat 384  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg 432  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct 480  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag 528



Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
				165					170						175	
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggt	gga	aat	cct	aaa	agt	gta	576
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
			195					200				205				
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
		210					215				220					
ggt	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggt	tgc	tct	aga	gag	aat	768
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	aac	cct	ttg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Asn	Pro	Leu	Ser	Val	
		275					280					285				
aac	ttt	ggt	ccg	acc	gtg	gat	ggt	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	

385	390	395	400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc				1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala				
405		410	415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa				1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu				
420	425		430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta				1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu				
435	440		445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt				1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser				
450	455		460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca				1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro				
465	470	475	480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act				1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr				
485	490		495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg				1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr				
500	505		510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa				1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys				
515	520		525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa				1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys				
530	535		540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa				1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln				
545	550	555	560	
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc				1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu				
565	570			
<210> 44				
<211> 574				
<212> PRT				
<213> Artificial Sequence				
<220>				
<223> synthetic butyrylcholinesterase variant				
<220>				
<221>VARIANT				
<222> 227				

&lt;223&gt; Xaa = Ala

&lt;400&gt; 44

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125		
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Asn	Pro	Leu	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365	
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395	400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430	

Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
           435                          440                          445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
           450                          455                          460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465                          470                          475                          480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
                           485                          490                          495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                           500                          505                          510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
                           515                          520                          525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
           530                          535                          540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545                          550                          555                          560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                           565                          570

<210> 45

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 45

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1                          5                          10                          15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20                          25                          30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35                          40                          45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50                          55                          60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65                          70                          75                          80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85                          90                          95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	

100	105	110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125			384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140			432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160			480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175			528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190			576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205			624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc cct gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Pro Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly			1008

325										330					335					
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa		1056			
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu					
			340					345					350							
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc		1104			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser					
		355					360					365								
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac		1152			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn					
	370					375					380									
tac	cgt	gag	gcc	ttg	ggt	gat	ggt	ggt	ggg	gat	tat	aat	ttc	ata	tgc		1200			
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys					
385					390					395					400					
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc		1248			
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala					
				405					410					415						
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa		1296			
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu					
			420					425					430							
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta		1344			
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu					
		435				440						445								
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt		1392			
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser					
	450				455						460									
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca		1440			
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro					
465					470					475					480					
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act		1488			
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr					
				485					490					495						
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg		1536			
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr					
			500					505					510							
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa		1584			
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys					
		515				520						525								
gtc	ttg	gaa	atg	aca	gga	aat	att	gat												

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

1722

&lt;210&gt; 46

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 46

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Pro Asp Met Pro Asp

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      290                      295                      300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly
305                      310                      315                      320
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly
      325                      330                      335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
      340                      345                      350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
      355                      360                      365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
      370                      375                      380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385                      390                      395                      400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
      405                      410                      415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
      420                      425                      430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
      435                      440                      445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
      450                      455                      460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465                      470                      475                      480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
      485                      490                      495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
      500                      505                      510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
      515                      520                      525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
      530                      535                      540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545                      550                      555                      560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
      565                      570

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&lt;210&gt; 47

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 47

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gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg      48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met
 1                      5                      10                      15

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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc      96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
      20                      25                      30

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tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816

Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg cgt cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Arg Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465 470 475 480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act	1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr	

485										490					495					
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536				
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr					
			500					505					510							
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584				
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys					
		515					520					525								
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632				
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys					
		530				535					540									
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa	1680				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln					
545					550					555					560					
ttt	aac	gat	tac	act	agc	aag	aaa	gaa	agt	tgt	gtg	ggg	ctc			1722				
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu							
				565					570											

&lt;210&gt; 48

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 48

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
1				5					10					15	
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
		50				55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75				80	
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120						125		
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
		130				135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln

				165					170					175			
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val		
			180						185					190			
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195					200					205					
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
	210					215					220						
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
225					230					235					240		
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		
				245					250					255			
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260						265					270			
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Arg	Pro	Leu	Ser	Val		
		275					280					285					
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp		
	290					295					300						
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly		
305					310					315					320		
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly		
			325						330					335			
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu		
			340						345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser		
		355					360					365					
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn		
	370					375					380						
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys		
385					390					395					400		
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
			405						410					415			
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu		
		420						425					430				
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
	435					440					445						
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
	450					455					460						
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470					475					480		
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		
			485						490					495			
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr		
		500						505					510				
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys		
		515					520					525					
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys		
	530					535					540						
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
545					550					555					560		
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu				
			565						570								

&lt;210&gt; 49

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 49

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	



195	200	205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg tct cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Ser Pro Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc tct gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Ser Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296

tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta 1344  
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
435 440 445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
450 455 460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
565 570

<210> 50

<211> 574

<212> PRT

### <213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

## <221>VARIANT

&lt;222&gt; 227

<223> Xaa = Ala

<400> 50

Glu 1	Asp	Asp	Ile	Ile 5	Ile	Ala	Thr	Lys	Asn 10	Gly	Lys	Val	Arg	Gly 15	Met
Asn	Leu	Thr	Val 20	Phe	Gly	Gly	Thr	Val 25	Thr	Ala	Phe	Leu	Gly 30	Ile	Pro
Tyr	Ala	Gln 35	Pro	Pro	Leu	Gly	Arg 40	Leu	Arg	Phe	Lys	Lys 45	Pro	Gln	Ser



Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Ser	Pro	Leu	Ser	Val	275	280	285
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Ser	Asp	Met	Pro	Asp	290	295	300
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	450	455	460
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	465	470	475
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	485	490	495
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr			



				500				505					510			
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	
	530					535					540					
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	
545					550					555					560	
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu			
				565					570							

```
<210> 51
<211> 1722
<212> DNA
<213> Artificial Sequence
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<220>
<221> CDS
<222> (1) ... (1722)
```

<223> synthetic butyrylcholinesterase variant

<400> 51																	
gaa	gat	gac	atc	ata	att	gca	aca	aag	aat	gga	aaa	gtc	aga	ggg	atg	48	
Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met		
1			5			10			15								
aac	ttg	aca	gtt	ttt	ggg	ggc	acg	gta	aca	gcc	ttt	ctt	gga	att	ccc	96	
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro		
20			25			30											
tat	gca	cag	cca	cct	ctt	ggg	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser		
35			40			45											
ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser		
50			55			60											
tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu		
65			70			75			80								
atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288	
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn		
85			90			95											
gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp		
100			105			110											
att	tat	ggg	ggg	ggg	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		
115			120			125											
gat	ggc	aag	ttt	ctg	gct	cgg	ggt	gaa	aga	ggt	att	gta	gtg	tca	atg	432	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met		
130			135			140											

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg tat cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Tyr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104

atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510	1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525	1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540	1632
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln 545 550 555 560	1680
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu 565 570	1722

&lt;210&gt; 52

&lt;211&gt; 573

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; (1)...(573)

&lt;223&gt; Xaa = Ala

&lt;400&gt; 52

Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	Asn
1				5					10					15	
Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	Tyr
		20						25					30		
Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	Leu
		35					40					45			
Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	Cys
	50					55					60				
Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	Met
65				70						75					80
Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val
			85					90						95	
Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	Ile
			100					105					110		
Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	Asp
	115						120					125			
Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	Asn
	130					135					140				
Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	Glu
145					150					155					160
Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	Trp
			165					170						175	
Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	Thr
			180					185					190		
Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	Leu
		195					200					205			
Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	Gly
	210					215					220				
Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	Asn
225					230					235					240
Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	Glu
			245						250					255	
Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	Leu
		260						265					270		
Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Tyr	Pro	Leu	Ser	Val	Asn
	275						280					285			
Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	Ile
	290					295					300				
Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	Val
305					310					315					320
Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	Phe
			325						330					335	
Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	Gly
			340					345					350		
Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	Ile
		355					360					365			
Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	Tyr

370	375	380
Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys Pro		
385	390	395
Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe		400
	405	410
Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp		415
	420	425
Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro		430
	435	440
Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg		445
	450	455
Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn		460
465	470	475
Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr Glu		480
	485	490
Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr Lys		495
	500	505
Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys Val		510
	515	520
Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala		525
	530	535
Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln Phe		540
545	550	555
Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu		560
	565	570

&lt;210&gt; 53

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 53

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act aat ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Asn Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	



ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggc tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510	1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525	1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa	1632

Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa .1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 54

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 54

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
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 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255

Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Asn Leu Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly  
 325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350  
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 55

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 55

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

48

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro 20 25 30	96
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser 35 40 45	144
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser 50 55 60	192
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu 65 70 75 80	240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95	288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110	336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125	384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720

aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cag ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Gln Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440

Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 56

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 56

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
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 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr

115					120					125					
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
130						135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225					230					235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
		260						265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Gln	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345				350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
				405					410					415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
		420					425					430			
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
		435				440					445				
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser
	450					455					460				
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro
465					470					475					480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr
				485					490					495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr
		500					505					510			
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
		515					520					525			
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys
	530					535					540				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln
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Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu		
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<210> 57  
 <211> 1722  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 57

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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	



tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggg tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct gcg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Ala Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248

Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
405 410 415

ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa 1296  
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
420 425 430

tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta 1344  
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
435 440 445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
450 455 460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
565 570

<210> 58

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221> VARIANT

<222> 227

<223> Xaa = Ala

<400> 58

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Ala	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365	
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395	400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430	
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445	
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser				

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      450                      455                      460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465                      470                      475                      480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
      485                      490                      495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
      500                      505                      510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
      515                      520                      525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
      530                      535                      540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545                      550                      555                      560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
      565                      570

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<210> 59

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 59

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gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg      48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met
 1                      5                      10                      15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc      96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
      20                      25                      30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct      144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
      35                      40                      45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct      192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
      50                      55                      60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag      240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu
      65                      70                      75                      80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat      288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn
      85                      90                      95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg      336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp
      100                      105                      110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat      384

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Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
	115						120					125				
gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					
aac	tat	agg	gtg	ggg	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	
gag	gct	cca	ggg	aac	atg	ggg	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
			165						170					175		
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggg	gga	aat	cct	aaa	agt	gta	576
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
		180						185					190			
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
	210					215					220					
ggg	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggg	tgc	tct	aga	gag	aat	768
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ggg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Gly	Ser	Val	
		275					280					285				
aac	ttt	ggg	ccg	acc	gtg	gat	ggg	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggg	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggg	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	

340	345	350	
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495			1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510			1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525			1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540			1632
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln 545 550 555 560			1680
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu 565 570			1722

<210> 60  
 <211> 574  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic butyrylcholinesterase variant

<220>  
 <221> VARIANT  
 <222> 227  
 <223> Xaa = Ala

<400> 60  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Gly Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly

				325						330						335			
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu				
			340					345					350						
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser				
		355					360					365							
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn				
	370					375					380								
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys				
385					390					395					400				
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala				
			405						410				415						
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu				
		420					425					430							
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu				
	435					440					445								
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser				
	450				455					460									
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro				
465					470				475					480					
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr				
			485						490					495					
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr				
		500					505					510							
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys				
	515					520					525								
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys				
	530				535				540										
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln				
545					550				555					560					
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu						
			565				570												

&lt;210&gt; 61

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 61

gaa	gat	gac	atc	ata	att	gca	aca	aag	aat	gga	aaa	gtc	aga	ggg	atg	48
Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	
1			5					10					15			

aac	ttg	aca	gtt	ttt	ggt	ggc	acg	gta	aca	gcc	ttt	ctt	gga	att	ccc	96
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	
		20					25					30				

tat	gca	cag	cca	cct	ctt	ggt	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35				40					45					

ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser		
50						55					60						
tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu		
65					70				75						80		
atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288	
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn		
				85					90					95			
gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp		
			100					105					110				
att	tat	ggt	ggt	ggt	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		
		115				120						125					
gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met		
	130					135					140						
aac	tat	agg	gtg	ggt	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro		
	145				150					155					160		
gag	gct	cca	ggg	aac	atg	ggt	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln		
			165						170					175			
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggt	gga	aat	cct	aaa	agt	gta	576	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val		
			180					185					190				
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195				200						205					
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
	210					215					220						
ggt	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
	225				230				235						240		
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggt	tgc	tct	aga	gag	aat	768	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		
			245					250						255			
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260					265					270				
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	aag	tca	gta	864	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Lys	Ser	Val		

275	280	285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
ggt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495			1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr			1536

500	505	510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa			1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys			
515	520	525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa			1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys			
530	535	540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa			1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln			
545	550	555	560
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc			1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu			
565	570		

&lt;210&gt; 62

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 62

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	

195	200	205
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser		
210	215	220
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg		
225	230	235
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn		
245	250	255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile		
260	265	270
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Lys Ser Val		
275	280	285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp		
290	295	300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly		
305	310	315
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly		
325	330	335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu		
340	345	350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser		
355	360	365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn		
370	375	380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys		
385	390	395
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala		
405	410	415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu		
420	425	430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu		
435	440	445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser		
450	455	460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro		
465	470	475
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr		
485	490	495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr		
500	505	510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys		
515	520	525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys		
530	535	540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln		
545	550	555
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu		
565	570	

&lt;210&gt; 63

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

## &lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 63

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	

210	215	220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct atg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Met Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tggt atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 64

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221> VARIANT

<222> 227

<223> Xaa = Ala

<400> 64

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90						95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
				165					170						175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
	210					215					220					
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
Glu	Thr	Glu	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260				265					270				
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Met	Ser	Val	
		275					280					285				
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390				395						400	
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
	450					455					460					
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470				475						480	
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490					495		
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
			500					505					510			
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	



530		535		540	
Ala Gly Phe His Arg Trp	Asn Asn Tyr Met Met	Asp Trp Lys Asn Gln			
545	550	555	560		
Phe Asn Asp Tyr Thr Ser	Lys Lys Glu Ser Cys	Val Gly Leu			
	565	570			

&lt;210&gt; 65

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 65

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tggttt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
gggtcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct aat tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Asn Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
gggtta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	

tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200.
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465 470 475 480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act	1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr	
485 490 495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg	1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr	
500 505 510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa	1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys	
515 520 525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa	1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys	
530 535 540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa	1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln	
545 550 555 560	
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc	1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu	
565 570	

&lt;210&gt; 66

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 66

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Asn	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365	
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395	400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415	

Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 67

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 67

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct cgt tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Arg Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	

gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465 470 475 480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act	1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr	
485 490 495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg	1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr	
500 505 510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa	1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys	
515 520 525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa	1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys	
530 535 540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa	1680

Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 68

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 68

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
1			5					10					15		
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
	115						120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180						185				190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225					230					235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Arg	Ser	Val
		275					280						285		



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Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp
290      295      300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly
305      310      315      320
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly
      325      330      335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
      340      345      350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
      355      360      365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
      370      375      380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385      390      395      400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
      405      410      415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
      420      425      430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
      435      440      445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
      450      455      460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465      470      475      480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
      485      490      495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
      500      505      510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
      515      520      525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
      530      535      540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545      550      555      560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
      565      570

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&lt;210&gt; 69

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 69

```

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met
1          5          10          15

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48

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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
      20          25          30

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96

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816

Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260					265					270				
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	ttt	gta	864	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Phe	Val		
		275					280					285					
aac	ttt	ggt	ccg	acc	gtg	gat	ggt	gat	ttt	ctc	act	gac	atg	cca	gac	912	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp		
	290					295					300						
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly		
305					310					315					320		
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008	
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly		
				325					330					335			
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu		
			340					345					350				
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser		
		355					360					365					
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152	
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn		
		370				375					380						
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys		
385					390					395					400		
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248	
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
				405					410					415			
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu		
			420					425					430				
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344	
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435				440						445					
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392	
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
		450				455					460						
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440	
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470					475					480		
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488	
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		

485	490	495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg			1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr			
500	505	510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa			1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys			
515	520	525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa			1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys			
530	535	540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa			1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln			
545	550	555	560
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc			1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu			
565	570		

&lt;210&gt; 70

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 70

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met			
1	5	10	15
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro			
20	25	30	
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser			
35	40	45	
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser			
50	55	60	
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu			
65	70	75	80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn			
85	90	95	
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp			
100	105	110	
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr			
115	120	125	
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met			
130	135	140	
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro			
145	150	155	160
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln			

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<210> 71
<211> 1722
<212> DNA
<213> Artificial Sequence
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<213> Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 71

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	

tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	

act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	

195	200	205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg cat gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu His Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
ggt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296

tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta 1344  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
           435                                  440                                  445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
           450                                  455                                  460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
           465                                  470                                  475                                  480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
                                   485                                  490                                  495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                                   500                                  505                                  510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
           515                                  520                                  525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
           530                                  535                                  540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
           545                                  550                                  555                                  560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                                   565                                  570

<210> 72

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 72

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
   1                  5                  10                  15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
           20                  25                  30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
           35                  40                  45



Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	His	Val	275	280	285
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	450	455	460
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	465	470	475
Asn	Glu	Thr	Gln	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		485	490	495
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr			



				500						505						510			
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys				
		515					520					525							
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys				
	530					535					540								
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln				
545					550					555					560				
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu						
				565					570										

&lt;210&gt; 73

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 73

gaa	gat	gac	atc	ata	att	gca	aca	aag	aat	gga	aaa	gtc	aga	ggg	atg	48
Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	
1				5					10					15		

aac	ttg	aca	gtt	ttt	ggt	ggc	acg	gta	aca	gcc	ttt	ctt	gga	att	ccc	96
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	
			20					25					30			

tat	gca	cag	cca	cct	ctt	ggt	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35					40					45				

ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50					55					60					

tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65				70					75						80	

atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
			85					90						95		

gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105						110		

att	tat	ggt	ggt	ggt	ttt	caa	act	gga	aca	tca	tct	tta	cat	ggt	tat	384
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				

gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg cgt gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Arg Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104

atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465 470 475 480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act	1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr	
485 490 495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg	1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr	
500 505 510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa	1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys	
515 520 525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa	1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys	
530 535 540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa	1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln	
545 550 555 560	
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc	1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu	
565 570	

&lt;210&gt; 74

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 74

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
1				5					10					15	
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100						105				110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120						125		
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
	195						200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230						235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Arg	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				

Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 75

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 75

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg act gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Thr Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	



ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
ggt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510	1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525	1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa	1632

Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 76

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 76

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
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 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255

Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Thr Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly  
 325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350  
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 77

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 77

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 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768

Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
			275				280					285				
aac	ttt	ggt	ccg	acc	gtg	gat	ggt	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	gct	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Ala	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345						350		
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
		450				455					460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	

465	470	475	480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act				1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr				
	485	490	495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg				1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr				
	500	505	510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa				1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys				
	515	520	525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa				1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys				
	530	535	540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa				1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln				
	545	550	555	560
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc				1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu				
	565	570		

&lt;210&gt; 78

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 78

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met				
1 5 10 15				
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro				
20 25 30				
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser				
35 40 45				
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser				
50 55 60				
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu				
65 70 75 80				
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn				
85 90 95				
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp				
100 105 110				
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr				
115 120 125				
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met				

130	135	140
Asn Tyr Arg Val Gly	Ala Leu Gly Phe Leu	Ala Leu Pro Gly Asn Pro
145	150	155
Glu Ala Pro Gly	Asn Met Gly Leu Phe Asp	Gln Gln Leu Ala Leu Gln
	165	170
Trp Val Gln Lys	Asn Ile Ala Ala Phe Gly	Gly Asn Pro Lys Ser Val
	180	185
Thr Leu Phe Gly	Glu Ser Ala Gly	Ala Ala Ser Val Ser Leu His Leu
	195	200
Leu Ser Pro Gly	Ser His Ser Leu Phe Thr	Arg Ala Ile Leu Gln Ser
	210	215
Gly Ser Xaa Asn	Ala Pro Trp Ala Val Thr	Ser Leu Tyr Glu Ala Arg
225	230	235
Asn Arg Thr Leu	Asn Leu Ala Lys Leu Thr	Gly Cys Ser Arg Glu Asn
	245	250
Glu Thr Glu Ile	Ile Lys Cys Leu Arg	Asn Lys Asp Pro Gln Glu Ile
	260	265
Leu Leu Asn Glu	Ala Phe Val Val Pro Tyr	Gly Thr Pro Leu Ser Val
	275	280
Asn Phe Gly Pro	Thr Val Asp Gly	Asp Phe Leu Thr Asp Met Pro Asp
	290	295
Ile Leu Leu Glu	Leu Gly Gln Phe Lys Lys	Thr Gln Ile Leu Val Gly
305	310	315
Val Asn Lys Asp	Glu Gly Ala Ala Phe Leu	Val Tyr Gly Ala Pro Gly
	325	330
Phe Ser Lys Asp	Asn Asn Ser Ile Ile Thr	Arg Lys Glu Phe Gln Glu
	340	345
Gly Leu Lys Ile	Phe Phe Pro Gly	Val Ser Glu Phe Gly Lys Glu Ser
	355	360
Ile Leu Phe His	Tyr Thr Asp Trp	Val Asp Asp Gln Arg Pro Glu Asn
	370	375
Tyr Arg Glu Ala	Leu Gly Asp Val	Val Gly Asp Tyr Asn Phe Ile Cys
385	390	395
Pro Ala Leu Glu	Phe Thr Lys Lys Phe Ser	Glu Trp Gly Asn Asn Ala
	405	410
Phe Phe Tyr Tyr	Phe Glu His Arg Ser	Ser Lys Leu Pro Trp Pro Glu
	420	425
Trp Met Gly Val	Met His Gly Tyr Glu	Ile Glu Phe Val Phe Gly Leu
	435	440
Pro Leu Glu Arg	Arg Asp Asn Tyr Thr	Lys Ala Glu Glu Ile Leu Ser
	450	455
Arg Ser Ile Val	Lys Arg Trp Ala Asn	Phe Ala Lys Tyr Gly Asn Pro
465	470	475
Asn Glu Thr Gln	Asn Asn Ser Thr Ser	Trp Pro Val Phe Lys Ser Thr
	485	490
Glu Gln Lys Tyr	Leu Thr Leu Asn Thr	Glu Ser Thr Arg Ile Met Thr
	500	505
Lys Leu Arg Ala	Gln Gln Cys Arg Phe	Trp Thr Ser Phe Phe Pro Lys
	515	520
Val Leu Glu Met	Thr Gly Asn Ile Asp	Glu Ala Glu Trp Glu Trp Lys
	530	535
Ala Gly Phe His	Arg Trp Asn Asn Tyr	Met Met Asp Trp Lys Asn Gln
545	550	555
Phe Asn Asp Tyr	Thr Ser Lys Lys Glu	Ser Cys Val Gly Leu
	565	570

<211> 1722  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 79

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat 384  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg 432  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct 480  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag 528  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175

tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta 576



Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
		210					215				220					
ggc	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggt	tgc	tct	aga	gag	aat	768
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
aac	ttt	ggt	ccg	acc	gtg	gat	ggt	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	cct	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Pro	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325				330					335			
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggc	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390				395						400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	

405	410	415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495			1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510			1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525			1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540			1632
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln 545 550 555 560			1680
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu 565 570			1722

&lt;210&gt; 80

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 80

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met

1	5	10	15
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro			
20		25	30
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser			
35		40	45
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser			
50		55	60
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu			
65		70	75
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn			
85		90	95
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp			
100		105	110
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr			
115		120	125
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met			
130		135	140
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro			
145		150	155
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln			
165		170	175
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val			
180		185	190
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu			
195		200	205
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser			
210		215	220
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg			
225		230	235
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn			
245		250	255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile			
260		265	270
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val			
275		280	285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp			
290		295	300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly			
305		310	315
Val Asn Lys Asp Glu Gly Pro Ala Phe Leu Val Tyr Gly Ala Pro Gly			
325		330	335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu			
340		345	350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser			
355		360	365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn			
370		375	380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys			
385		390	395
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala			
405		410	415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu			
420		425	430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu			
435		440	445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser			
450		455	460

Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 81

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 81

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat 384  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr

115	120	125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140			432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160			480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175			528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190			576
act ctg ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205			624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctg act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ctt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Leu Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056

ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510	1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525	1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540	1632
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln 545 550 555 560	1680
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu 565 570	1722

<210> 82  
 <211> 574  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic butyrylcholinesterase variant

<220>  
 <221>VARIANT  
 <222> 227  
 <223> Xaa = Ala

<400> 82  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
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 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
           20                  25                  30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
           35                  40                  45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
   50                  55                  60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65                  70                  75                  80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
           85                  90                  95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
           100                  105                  110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
   115                  120                  125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
   130                  135                  140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145                  150                  155                  160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
           165                  170                  175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
           180                  185                  190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
   195                  200                  205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
   210                  215                  220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225                  230                  235                  240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
           245                  250                  255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
           260                  265                  270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val  
   275                  280                  285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
   290                  295                  300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305                  310                  315                  320  
 Val Asn Lys Asp Glu Gly Thr Ala Leu Leu Val Tyr Gly Ala Pro Gly  
           325                  330                  335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu

			340					345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
	450					455					460					
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490					495		
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
			500					505					510			
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	
	530					535					540					
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	
545					550					555					560	
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu			
				565				570								

<210> 83

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (1722)$ 

<223> synthetic butyrylcholinesterase variant

<400> 83

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
20 25 30

tat	gca	cag	cca	cct	ctt	ggt	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35				40					45					

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat qca aat tct 192



Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
50						55					60					
tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65					70					75					80	
atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		
gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			
att	tat	ggg	ggg	ggg	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				
gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					
aac	tat	agg	gtg	ggg	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	
gag	gct	cca	ggg	aac	atg	ggg	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
				165					170					175		
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggg	gga	aat	cct	aaa	agt	gta	576
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
	210						215				220					
ggg	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggg	tgc	tct	aga	gag	aat	768
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	

275	280	285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
ggt aat aaa gat gaa ggg aca gct ttt tcg gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Ser Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495			1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510			1536

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
           515                          520                          525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
           530                          535                          540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
           545                          550                          555                          560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                                   565                                  570

<210> 84

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221> VARIANT

<222> 227

<223> Xaa = Ala

<400> 84

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
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 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
           20                  25                  30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
           35                  40                  45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
           50                  55                  60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
   65                  70                  75                  80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
           85                  90                  95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
           100                  105                  110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
           115                  120                  125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
           130                  135                  140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
   145                  150                  155                  160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
           165                  170                  175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
           180                  185                  190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
           195                  200                  205

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Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser
210                               215                               220
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg
225                               230                               235                               240
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn
245                               250                               255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile
260                               265                               270
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val
275                               280                               285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp
290                               295                               300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly
305                               310                               315                               320
Val Asn Lys Asp Glu Gly Thr Ala Phe Ser Val Tyr Gly Ala Pro Gly
325                               330                               335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
340                               345                               350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
355                               360                               365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
370                               375                               380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385                               390                               395                               400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
405                               410                               415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
420                               425                               430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
435                               440                               445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
450                               455                               460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465                               470                               475                               480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
485                               490                               495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
500                               505                               510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
515                               520                               525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
530                               535                               540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545                               550                               555                               560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
565                               570

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&lt;210&gt; 85

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 85

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	

ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230, 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gcg tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Ala Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 86

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221> VARIANT

<222> 227

<223> Xaa = Ala

<400> 86

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 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu

65				70					75				80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr
				85					90				95
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu
			100					105				110	Trp
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His
		115					120					125	Val
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val
		130				135					140		Ser
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly
145					150				155				Asn
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala
				165					170				Leu
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys
			180						185				Ser
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu
		195					200					205	His
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu
		210				215							Gln
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu
225					230					235			Ala
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg
				245					250				Glu
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln
			260					265					Ile
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu
		275					280					285	Ser
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met
		290				295					300		Pro
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu
305					310				315				Val
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Ala	Tyr	Gly	Ala
			325						330				Pro
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe
		340						345					Gln
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys
		355					360					365	Glu
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro
		370				375					380		Glu
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe
385					390				395				Ile
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn
				405					410				Ala
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp
		420						425				430	Pro
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe
		435				440						445	Gly
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile
		450				455					460		Leu
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly
465					470				475				Asn
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys
				485					490				Ser
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile
			500					505				510	Met
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe
		515					520					525	Lys



Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 87

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 87

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 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat 384  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg 432  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct 480  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro

145	150	155	160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag				528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln				
	165	170	175	
tggt gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta				576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val				
	180	185	190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg				624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu				
	195	200	205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt				672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser				
210	215	220		
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg				720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg				
225	230	235	240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat				768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn				
	245	250	255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att				816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile				
	260	265	270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta				864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val				
	275	280	285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac				912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp				
	290	295	300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt				960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly				
305	310	315	320	
gtt aat aaa gat gaa ggg aca gct ttt tta ggt tat ggt gct cct ggc				1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Gly Tyr Gly Ala Pro Gly				
	325	330	335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa				1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu				
	340	345	350	
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc				1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser				
	355	360	365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac				1152

Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn		
370						375					380						
tac	cgt	gag	gcc	ttg	ggg	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys		
385					390					395					400		
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248	
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
				405					410					415			
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu		
			420					425					430				
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggg	tta	1344	
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435					440					445					
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392	
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
		450				455					460						
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440	
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470					475					480		
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488	
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		
				485					490					495			
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr		
			500					505					510				
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584	
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys		
		515					520					525					
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632	
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys		
		530				535					540						
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa	1680	
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
545					550					555					560		
ttt	aac	gat	tac	act	agc	aag	aaa	gaa	agt	tgt	gtg	ggg	ctc			1722	
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu				
				565					570								

&lt;210&gt; 88

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 88

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
1				5					10					15	
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
	35						40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
	195						200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225					230					235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Gly	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys

385                      390                      395                      400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
                                  405                      410                      415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
                                  420                      425                      430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
                                  435                      440                      445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
                                  450                      455                      460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465                      470                      475                      480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
                                  485                      490                      495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                                  500                      505                      510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
                                  515                      520                      525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
                                  530                      535                      540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545                      550                      555                      560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                                  565                      570

<210> 89

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 89

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg                      48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
   1                      5                      10                      15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc                      96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
                                  20                      25                      30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct                      144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
                                  35                      40                      45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct                      192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
                                  50                      55                      60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag                      240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
   65                      70                      75                      80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat                      288

Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn		
				85					90						95		
gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp		
			100					105					110				
att	tat	ggt	ggt	ggt	ttt	caa	act	gga	aca	tca	tct	tta	cat	ggt	tat	384	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		
		115					120						125				
gat	ggc	aag	ttt	ctg	gct	cgg	ggt	gaa	aga	ggt	att	gta	gtg	tca	atg	432	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met		
	130					135					140						
aac	tat	agg	gtg	ggt	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro		
145					150					155					160		
gag	gct	cca	ggg	aac	atg	ggt	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln		
				165					170					175			
tgg	ggt	caa	aaa	aat	ata	gca	gcc	ttt	ggt	gga	aat	cct	aaa	agt	gta	576	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val		
			180					185					190				
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	ggt	agc	ctg	cat	ttg	624	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195					200					205					
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
		210					215				220						
ggt	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
225					230					235					240		
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggt	tgc	tct	aga	gag	aat	768	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		
				245					250					255			
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260					265					270				
ctt	ctg	aat	gaa	gca	ttt	ggt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val		
		275					280					285					
aac	ttt	ggt	ccg	acc	gtg	gat	ggt	gat	ttt	ctc	act	gac	atg	cca	gac	912	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp		
	290					295					300						
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly		

305	310	315	320	
gtt aat aaa gat gaa ggg aca gct ttt tta cct tat ggt cct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Pro Tyr Gly Pro Pro Gly 325 330 335				1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350				1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365				1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380				1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400				1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415				1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430				1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445				1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460				1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480				1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495				1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510				1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525				1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540				1632

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 90

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 90

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270	



Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Pro Tyr Gly Pro Pro Gly  
 325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350  
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 91

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 91

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro

20	25	30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser 35 40 45			144
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser 50 55 60			192
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu 65 70 75 80			240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95			288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110			336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125			384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140			432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160			480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175			528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190			576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205			624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768

gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ott ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta tct tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Ser Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
                   485                                  490                                  495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                   500                                  505                                  510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
                   515                                  520                                  525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
                   530                                  535                                  540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
                   545                                  550                                  555                                  560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                   565                                  570

<210> 92

<211> 573

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> (1)...(573)

<223> Xaa = Ala

<400> 92

Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met Asn  
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 Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro Tyr  
                   20                                  25                                  30  
 Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu  
                   35                                  40                                  45  
 Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser Cys  
                   50                                  55                                  60  
 Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu Met  
   65                                  70                                  75                                  80  
 Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn Val  
                   85                                  90                                  95  
 Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp Ile  
                   100                                  105                                  110  
 Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr Asp  
                   115                                  120                                  125  
 Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met Asn  
                   130                                  135                                  140

Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro Glu  
 145 150 155 160  
 Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln Trp  
 165 170 175  
 Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val Thr  
 180 185 190  
 Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu Leu  
 195 200 205  
 Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser Gly  
 210 215 220  
 Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg Asn  
 225 230 235 240  
 Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn Glu  
 245 250 255  
 Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile Leu  
 260 265 270  
 Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val Asn  
 275 280 285  
 Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp Ile  
 290 295 300  
 Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly Val  
 305 310 315 320  
 Asn Lys Asp Glu Gly Thr Ala Phe Leu Ser Tyr Gly Ala Pro Gly Phe  
 325 330 335  
 Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu Gly  
 340 345 350  
 Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser Ile  
 355 360 365  
 Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr  
 370 375 380  
 Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys Pro  
 385 390 395 400  
 Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe  
 405 410 415  
 Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp  
 420 425 430  
 Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro  
 435 440 445  
 Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg  
 450 455 460  
 Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn  
 465 470 475 480  
 Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr Glu  
 485 490 495  
 Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr Lys  
 500 505 510  
 Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys Val  
 515 520 525  
 Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala  
 530 535 540  
 Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln Phe  
 545 550 555 560  
 Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

&lt;210&gt; 93

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 93

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	

act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggc tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta act tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Thr Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggc tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	

ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa 1296  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta 1344  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 94

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 94

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
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 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro



			20					25					30			
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35					40					45				
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50					55					60					
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65					70					75					80	
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			
Ile	Tyr	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Ser	Leu	His	Val	Tyr	
		115				120						125				
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
				165					170					175		
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
	210					215					220					
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Thr	Tyr	Gly	Ala	Pro	Gly	
			325						330					335		
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375										

Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 95

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 95

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 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat 384  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc gcg ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Ala Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104

Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser		
		355					360					365					
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152	
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn		
	370					375					380						
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys		
385					390				395						400		
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248	
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
				405					410					415			
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu		
			420					425					430				
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344	
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435					440					445					
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392	
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
		450				455					460						
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440	
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470					475					480		
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488	
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		
				485					490					495			
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr		
			500					505					510				
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584	
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys		
		515					520					525					
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632	
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys		
		530				535					540						
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa	1680	
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
545					550					555					560		
ttt	aac	gat	tac	act	agc	aag	aaa	gaa	agt	tgt	gtg	ggt	ctc			1722	
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu				
				565					570								

&lt;210&gt; 96

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 96

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
1			5						10					15	
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65				70						75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
	115						120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145				150						155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230						235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Ala	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser

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      355              360              365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
      370              375              380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385              390              395              400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
      405              410              415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
      420              425              430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
      435              440              445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
      450              455              460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465              470              475              480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
      485              490              495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
      500              505              510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
      515              520              525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
      530              535              540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545              550              555              560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
      565              570

```

&lt;210&gt; 97

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 97

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gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg      48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met
1              5              10              15

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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc      96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
      20              25              30

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```

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct      144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
      35              40              45

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ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct      192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
      50              55              60

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tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag      240

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Cys 65	Cys	Gln	Asn	Ile	Asp 70	Gln	Ser	Phe	Pro	Gly 75	Phe	His	Gly	Ser	Glu 80	
atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		
gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			
att	tat	ggg	ggg	ggg	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				
gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					
aac	tat	agg	gtg	ggg	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	
gag	gct	cca	ggg	aac	atg	ggg	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
			165						170					175		
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggg	gga	aat	cct	aaa	agt	gta	576
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
		210					215				220					
ggg	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggg	tgc	tct	aga	gag	aat	768
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
aac	ttt	ggg	ccg	acc	gtg	gat	ggg	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	

290	295	300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
ggt aat aaa gat gaa ggg aca gct ttt tta gtc ggg ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Gly Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495			1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510			1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525			1584



gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 98

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 98

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240

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Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn
      245      250      255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile
      260      265      270
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val
      275      280      285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp
      290      295      300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly
305      310      315
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Gly Gly Ala Pro Gly
      325      330      335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
      340      345      350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
      355      360      365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
      370      375      380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385      390      395
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
      405      410      415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
      420      425      430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
      435      440      445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
      450      455      460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465      470      475
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
      485      490      495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
      500      505      510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
      515      520      525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
      530      535      540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545      550      555
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
      565      570

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<210> 99

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 99

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gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met

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1	5	10	15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc				96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro				
20		25	30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct				144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser				
35		40	45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct				192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser				
50		55	60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag				240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu				
65		70	75	80
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat				288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn				
85		90	95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg				336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp				
100		105	110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat				384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr				
115		120	125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg				432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met				
130		135	140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct				480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro				
145		150	155	160
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag				528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln				
165		170	175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta				576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val				
180		185	190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg				624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu				
195		200	205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt				672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser				
210		215	220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg				720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg				
225		230	235	240

aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc ttg ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Leu Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 100

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221> VARIANT

<222> 227

<223> Xaa = Ala

<400> 100

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 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr

115	120	125
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met		
130	135	140
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro		
145	150	155
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln		
165	170	175
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val		
180	185	190
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu		
195	200	205
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser		
210	215	220
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg		
225	230	235
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn		
245	250	255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile		
260	265	270
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val		
275	280	285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp		
290	295	300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly		
305	310	315
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Leu Gly Ala Pro Gly		
325	330	335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu		
340	345	350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser		
355	360	365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn		
370	375	380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys		
385	390	395
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala		
405	410	415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu		
420	425	430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu		
435	440	445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser		
450	455	460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro		
465	470	475
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr		
485	490	495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr		
500	505	510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys		
515	520	525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys		
530	535	540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln		
545	550	555
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu		
565	570	

<210> 101  
 <211> 1722  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 101

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Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	

tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct oct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
ggt aat aaa gat gaa ggg aca gct ttt tta gtc tct ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Ser Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc agc aag tca gaa tgg gga aat aat gcc	1248



Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
				405					410						415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu		
			420					425					430				
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344	
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435					440					445					
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392	
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
		450				455					460						
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440	
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470					475					480		
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488	
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		
			485						490					495			
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr		
			500					505					510				
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584	
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys		
		515				520						525					
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632	
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys		
		530				535					540						
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa	1680	
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
545					550				555					560			
ttt	aac	gat	tac	act	agc	aag	aaa	gaa	agt	tgt	gtg	ggt	ctc			1722	
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu				
				565					570								

&lt;210&gt; 102

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 102

Glu 1	Asp	Asp	Ile	Ile 5	Ile	Ala	Thr	Lys	Asn 10	Gly	Lys	Val	Arg	Gly 15	Met
Asn	Leu	Thr	Val 20	Phe	Gly	Gly	Thr	Val 25	Thr	Ala	Phe	Leu	Gly 30	Ile	Pro
Tyr	Ala	Gln	Pro 35	Pro	Leu	Gly	Arg 40	Leu	Arg	Phe	Lys	Lys 45	Pro	Gln	Ser
Leu	Thr 50	Lys	Trp	Ser	Asp	Ile 55	Trp	Asn	Ala	Thr	Lys 60	Tyr	Ala	Asn	Ser
Cys 65	Cys	Gln	Asn	Ile	Asp 70	Gln	Ser	Phe	Pro	Gly 75	Phe	His	Gly	Ser	Glu
Met	Trp	Asn	Pro 85	Asn	Thr	Asp	Leu	Ser	Glu 90	Asp	Cys	Leu	Tyr	Leu 95	Asn
Val	Trp	Ile	Pro 100	Ala	Pro	Lys	Pro	Lys 105	Asn	Ala	Thr	Val	Leu 110	Ile	Trp
Ile	Tyr	Gly 115	Gly	Gly	Phe	Gln	Thr 120	Gly	Thr	Ser	Ser 125	Leu	His	Val	Tyr
Asp	Gly 130	Lys	Phe	Leu	Ala	Arg 135	Val	Glu	Arg	Val	Ile 140	Val	Val	Ser	Met
Asn 145	Tyr	Arg	Val	Gly	Ala 150	Leu	Gly	Phe	Leu	Ala 155	Leu	Pro	Gly	Asn 160	Pro
Glu	Ala	Pro	Gly 165	Asn	Met	Gly	Leu	Phe	Asp 170	Gln	Gln	Leu	Ala 175	Leu	Gln
Trp	Val	Gln	Lys 180	Asn	Ile	Ala	Ala	Phe 185	Gly	Gly	Asn	Pro	Lys 190	Ser	Val
Thr	Leu	Phe 195	Gly	Glu	Ser	Ala 200	Gly	Ala	Ala	Ser	Val 205	Ser	Leu	His	Leu
Leu	Ser 210	Pro	Gly	Ser	His	Ser 215	Leu	Phe	Thr	Arg	Ala 220	Ile	Leu	Gln	Ser
Gly 225	Ser	Xaa	Asn	Ala	Pro 230	Trp	Ala	Val	Thr	Ser 235	Leu	Tyr	Glu	Ala 240	Arg
Asn	Arg	Thr	Leu 245	Asn	Leu	Ala	Lys	Leu	Thr 250	Gly	Cys	Ser	Arg	Glu 255	Asn
Glu	Thr	Glu	Ile 260	Ile	Lys	Cys	Leu	Arg 265	Asn	Lys	Asp	Pro	Gln 270	Glu	Ile
Leu	Leu	Asn 275	Glu	Ala	Phe	Val	Val 280	Pro	Tyr	Gly	Thr 285	Pro	Leu	Ser	Val
Asn	Phe 290	Gly	Pro	Thr	Val 295	Asp	Gly	Asp	Phe	Leu 300	Thr	Asp	Met	Pro	Asp
Ile 305	Leu	Leu	Glu	Leu	Gly 310	Gln	Phe	Lys	Lys 315	Thr	Gln	Ile	Leu	Val 320	Gly
Val	Asn	Lys	Asp 325	Glu	Gly	Thr	Ala	Phe 330	Leu	Val	Ser	Gly	Ala 335	Pro	Gly
Phe	Ser	Lys	Asp 340	Asn	Asn	Ser	Ile 345	Ile	Thr	Arg	Lys	Glu	Phe 350	Gln	Glu
Gly	Leu	Lys 355	Ile	Phe	Phe	Pro	Gly 360	Val	Ser	Glu	Phe 365	Gly	Lys	Glu	Ser
Ile	Leu 370	Phe	His	Tyr	Thr 375	Asp	Trp	Val	Asp	Asp 380	Gln	Arg	Pro	Glu	Asn
Tyr 385	Arg	Glu	Ala	Leu	Gly 390	Asp	Val	Val	Gly	Asp 395	Tyr	Asn	Phe	Ile	Cys
Pro	Ala	Leu	Glu 405	Phe	Thr	Lys	Lys	Phe 410	Ser	Glu	Trp	Gly	Asn 415	Asn	Ala
Phe	Phe	Tyr 420	Tyr	Phe	Glu	His	Arg 425	Ser	Ser	Lys	Leu	Pro	Trp 430	Pro	Glu
Trp	Met	Gly 435	Val	Met	His	Gly 440	Tyr	Glu	Ile	Glu	Phe 445	Val	Phe	Gly	Leu
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser

450					455					460						
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490					495		
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
			500					505					510			
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	
		530				535					540					
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	
545					550					555					560	

Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
565 570

<210> 103

<211>, 1722

<212> DNA

### <213>. Artificial Sequence

 $\langle 220 \rangle$ 

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (1722)$ 

<223> synthetic butyrylcholinesterase variant

<400> 103

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Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
20 25 30

tat	gca	cag	cca	cct	ctt	ggt	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35				40						45				

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
50 55 60

tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65					70					75					80	

atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
100 105 110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tggt gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tgg ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Trp Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056

Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390				395						400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405				410						415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
		420						425					430			
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
	435					440						445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
	450				455						460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470				475						480	
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485				490						495		
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
		500						505					510			
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	
	530					535					540					
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa	1680
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	
545					550					555					560	
ttt	aac	gat	tac	act	agc	aag	aaa	gaa	agt	tgt	gtg	ggt	ctc			1722
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu			

565

570

<210> 104  
 <211> 574  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic butyrylcholinesterase variant

<220>  
 <221>VARIANT  
 <222> 227  
 <223> Xaa = Ala

<400> 104  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Trp Gly Ala Pro Gly

325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350  
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

&lt;210&gt; 105

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 105

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser 50 55 60	192
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu 65 70 75 80	240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95	288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110	336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125	384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816



ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt aag tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Lys Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg	1536

Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
565 570

<210> 106

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 106

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
1 5 10 15  
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
20 25 30  
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
35 40 45  
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
50 55 60  
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
65 70 75 80  
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
85 90 95  
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
100 105 110  
Ile Tyr Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
115 120 125  
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
130 135 140  
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
145 150 155 160  
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
165 170 175  
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
180 185 190

Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195					200					205					
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
		210				215					220						
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
225					230					235					240		
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		
				245						250					255		
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260					265						270			
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val		
		275					280							285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp		
		290				295						300					
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly		
305					310					315					320		
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly		
				325						330					335		
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu		
			340						345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser		
		355					360					365					
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn		
		370				375					380						
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys		
385					390					395					400		
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
				405						410					415		
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Lys	Trp	Pro	Glu		
			420					425						430			
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435					440							445			
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
		450				455								460			
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470					475					480		
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		
				485					490					495			
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr		
			500					505					510				
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys		
		515					520						525				
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys		
		530				535							540				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
545					550					555					560		
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu				
				565					570								

&lt;210&gt; 107

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

## &lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 107

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat 384  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg 432  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct 480  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag 528  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175

tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta 576  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190

act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg 624  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205

ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ttg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Leu Trp Pro Glu 420 425 430	1296

tgg	atg	gga	.gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta		1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	.	
		435					440					445					

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
450 455 460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
565 570

<210> 108

<211> 574

&lt;212&gt; PRT

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> synthetic butyrylcholinesterase variant

<220>

&lt;221&gt;VARIANT

&lt;222&gt; 227

<223> Xaa = Ala

 $\langle 400 \rangle \quad 108$ 

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
1 5 10 15

Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
20 25 30

Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
35 40 45

Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Leu	Trp	Pro	Glu	420	425	430
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	450	455	460
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	465	470	475
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	485	490	495
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr			

			500					505					510				
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys		
		515					520					525					
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys		
	530					535					540						
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
545					550					555					560		
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu				
				565					570								

&lt;210&gt; 109

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 109

gaa	gat	gac	atc	ata	att	gca	aca	aag	aat	gga	aaa	gtc	aga	ggg	atg	48
Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	
1				5					10					15		

aac	ttg	aca	gtt	ttt	ggt	ggc	acg	gta	aca	gcc	ttt	ctt	gga	att	ccc	96
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	
			20					25					30			

tat	gca	cag	cca	cct	ctt	ggt	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35				40						45				

ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50					55					60					

tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
	65				70					75					80	

atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		

gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			

att	tat	ggt	ggt	ggt	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115				120						125				

gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					



aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104

atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt cag tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Gln Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465 470 475 480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act	1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr	
485 490 495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg	1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr	
500 505 510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa	1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys	
515 520 525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa	1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys	
530 535 540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa	1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln	
545 550 555 560	
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc	1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu	
565 570	

&lt;210&gt; 110

&lt;211&gt; 573

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; (1)...(573)

&lt;223&gt; Xaa = Ala

&lt;400&gt; 110

Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	Asn	
1				5					10					15		
Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	Tyr	
		20						25					30			
Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	Leu	
		35					40					45				
Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	Cys	
	50					55					60					
Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	Met	
65					70					75					80	
Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	
			85						90					95		
Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	Ile	
			100					105					110			
Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	Asp	
		115					120					125				
Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	Asn	
	130					135					140					
Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	Glu	
145					150					155					160	
Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	Trp	
			165						170					175		
Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	Thr	
			180					185					190			
Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	Leu	
		195					200						205			
Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	Gly	
	210					215					220					
Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	Asn	
225					230					235					240	
Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	Glu	
			245						250				255			
Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	Leu	
		260						265					270			
Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	Asn	
	275						280					285				
Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	Ile	
	290					295					300					
Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	Val	
305					310					315					320	
Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	Phe	
			325						330				335			
Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	Gly	
		340						345					350			
Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	Ile	
	355					360						365				
Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	Tyr	
	370					375					380					

Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys Pro  
 385 390 395 400  
 Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe  
 405 410 415  
 Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Gln Trp Pro Glu Trp  
 420 425 430  
 Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro  
 435 440 445  
 Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg  
 450 455 460  
 Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn  
 465 470 475 480  
 Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr Glu  
 485 490 495  
 Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr Lys  
 500 505 510  
 Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys Val  
 515 520 525  
 Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala  
 530 535 540  
 Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln Phe  
 545 550 555 560  
 Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 111

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 111

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggg tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960

Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	agg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Arg	Trp	Pro	Glu	
			420					425					430			
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
		450				455					460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490				495			
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
			500					505					510			
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	

530

535

540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

&lt;210&gt; 112

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 112

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255

Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly  
 325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350  
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Arg Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 113

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 113

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15



aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	

aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt tcg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Ser Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440

Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 114

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221> VARIANT

<222> 227

<223> Xaa = Ala

<400> 114

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
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Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110

Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125

Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Ser	Trp	Pro	Glu	420	425	430
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	450	455	460
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	465	470	475
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	485	490	495
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	500	505	510
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	515	520	525
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	530	535	540
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	545	550	555
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu			565	570	

<210> 115  
 <211> 1722  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 115  
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 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat 384  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg 432  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct 480  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag 528  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175

tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta 576

Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
		210				215					220					
ggt	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggt	tgc	tct	aga	gag	aat	768
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
aac	ttt	ggt	ccg	acc	gtg	gat	ggt	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345						350		
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248

Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
				405					410						415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	acg	tgg	cca	gaa		1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Thr	Trp	Pro	Glu		
			420					425					430				
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggg	tta		1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435					440					445					
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt		1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
		450				455					460						
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca		1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470				475						480		
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act		1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		
			485						490					495			
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg		1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr		
			500					505					510				
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa		1584
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys		
		515					520					525					
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa		1632
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys		
	530					535					540						
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa		1680
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
545					550				555						560		
ttt	aac	gat	tac	act	agc	aag	aaa	gaa	agt	tgt	gtg	ggg	ctc				1722
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu				
			565					570									

&lt;210&gt; 116

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 116

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		115	120	125	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365	
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395	400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Thr	Trp	Pro	Glu	420	425	430	
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445	
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser				



450	455	460
Arg Ser Ile Val Lys	Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465	470	475
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr		480
	485	490
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr		495
	500	505
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys		510
	515	520
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys		525
	530	535
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln		540
545	550	555
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu		560
	565	570

&lt;210&gt; 117

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 117

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056

Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	gtt	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Val	Trp	Pro	Glu	
			420					425					430			
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
		450				455					460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490					495		
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
			500					505					510			
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	
		530				535					540					
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa	1680
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	
545					550					555					560	
ttt	aac	gat	tac	act	agc	aag	aaa	gaa	agt	tgt	gtg	ggt	ctc			1722

Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
565 570

<210> 118

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 118

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320

Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly  
 325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350  
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Val Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

&lt;210&gt; 119

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 119

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca gcc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat gcc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864

Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
aac	ttt	ggt	ccg	acc	gtg	gat	ggt	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295				300						
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340						345					350		
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	atg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Met	Pro	Glu	
			420					425					430			
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435				440						445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
		450				455					460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490					495		
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	

500	505	510	
aaa cta cgt gct caa caa tgt cga ttc tgg acā tca ttt ttt cca aaa			1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys			
515	520	525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa			1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys			
530	535	540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa			1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln			
545	550	555	560
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc			1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu			
565	570		

&lt;210&gt; 120

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 120

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	



195	200	205
Leu Ser Pro Gly Ser His Ser	Leu Phe Thr Arg Ala	Ile Leu Gln Ser
210	215	220
Gly Ser Xaa Asn Ala Pro Trp	Ala Val Thr Ser Leu	Tyr Glu Ala Arg
225	230	235
Asn Arg Thr Leu Asn Leu Ala	Lys Leu Thr Gly Cys	Ser Arg Glu Asn
245	250	255
Glu Thr Glu Ile Ile Lys Cys	Leu Arg Asn Lys Asp	Pro Gln Glu Ile
260	265	270
Leu Leu Asn Glu Ala Phe Val	Val Pro Tyr Gly Thr	Pro Leu Ser Val
275	280	285
Asn Phe Gly Pro Thr Val Asp	Gly Asp Phe Leu Thr	Asp Met Pro Asp
290	295	300
Ile Leu Leu Glu Leu Gly Gln	Phe Lys Lys Thr Gln	Ile Leu Val Gly
305	310	315
Val Asn Lys Asp Glu Gly Thr	Ala Phe Leu Val Tyr	Gly Ala Pro Gly
325	330	335
Phe Ser Lys Asp Asn Asn Ser	Ile Ile Thr Arg Lys	Glu Phe Gln Glu
340	345	350
Gly Leu Lys Ile Phe Phe Pro	Gly Val Ser Glu Phe	Gly Lys Glu Ser
355	360	365
Ile Leu Phe His Tyr Thr Asp	Trp Val Asp Asp Gln	Arg Pro Glu Asn
370	375	380
Tyr Arg Glu Ala Leu Gly Asp	Val Val Gly Asp Tyr	Asn Phe Ile Cys
385	390	395
Pro Ala Leu Glu Phe Thr Lys	Lys Phe Ser Glu Trp	Gly Asn Asn Ala
405	410	415
Phe Phe Tyr Tyr Phe Glu His	Arg Ser Ser Lys Leu	Pro Met Pro Glu
420	425	430
Trp Met Gly Val Met His Gly	Tyr Glu Ile Glu Phe	Val Phe Gly Leu
435	440	445
Pro Leu Glu Arg Arg Asp Asn	Tyr Thr Lys Ala Glu	Glu Ile Leu Ser
450	455	460
Arg Ser Ile Val Lys Arg Trp	Ala Asn Phe Ala Lys	Tyr Gly Asn Pro
465	470	475
Asn Glu Thr Gln Asn Asn Ser	Thr Ser Trp Pro Val	Phe Lys Ser Thr
485	490	495
Glu Gln Lys Tyr Leu Thr Leu	Asn Thr Glu Ser Thr	Arg Ile Met Thr
500	505	510
Lys Leu Arg Ala Gln Gln Cys	Arg Phe Trp Thr Ser	Phe Phe Pro Lys
515	520	525
Val Leu Glu Met Thr Gly Asn	Ile Asp Glu Ala Glu	Trp Glu Trp Lys
530	535	540
Ala Gly Phe His Arg Trp Asn	Asn Tyr Met Met Asp	Trp Lys Asn Gln
545	550	555
Phe Asn Asp Tyr Thr Ser Lys	Lys Glu Ser Cys Val	Gly Leu
565	570	

&lt;210&gt; 121

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

## &lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 121

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	

210	215	220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tat cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Tyr Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 122

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221> VARIANT

<222> 227

<223> Xaa = Ala

<400> 122

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn		
				85					90					95			
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp		
			100					105					110				
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		
		115					120					125					
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met		
		130				135					140						
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro		
145					150					155					160		
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln		
				165					170						175		
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val		
			180					185					190				
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195					200					205					
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
		210				215					220						
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
225				230					235						240		
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		
				245					250					255			
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260					265					270				
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val		
			275				280					285					
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp		
		290				295					300						
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly		
305					310					315					320		
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly		
			325						330					335			
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu		
			340					345					350				
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser		
		355					360					365					
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn		
			370			375					380						
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys		
385					390					395					400		
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
				405					410					415			
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Tyr	Pro	Glu		
			420					425					430				
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435					440						445				
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
		450				455						460					
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470					475					480		
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		
				485					490					495			
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr		
			500					505					510				
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys		
		515					520					525					
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys		

530		535		540
Ala Gly Phe His Arg Trp	Asn Asn Tyr Met Met	Asp Trp Lys Asn Gln		
545	550	555	560	
Phe Asn Asp Tyr Thr Ser	Lys Lys Glu Ser Cys	Val Gly Leu		
	565	570		

&lt;210&gt; 123

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 123

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tggttt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
actctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctttct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
gggtcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aacaga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gagact gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
cttctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aacttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gttaat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttcagc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
gggtta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atcctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	

tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cag gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Gln Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465 470 475 480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act	1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr	
485 490 495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg	1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr	
500 505 510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa	1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys	
515 520 525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa	1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys	
530 535 540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa	1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln	
545 550 555 560	
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc	1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu	
565 570	

&lt;210&gt; 124

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;



<221>VARIANT

&lt;222&gt; 227

<223> Xaa = Ala

<400> 124

Glu 1	Asp	Asp	Ile	Ile 5	Ile	Ala	Thr	Lys	Asn 10	Gly	Lys	Val	Arg	Gly 15	Met
Asn	Leu	Thr	Val 20	Phe	Gly	Gly	Thr	Val 25	Thr	Ala	Phe	Leu	Gly 30	Ile	Pro
Tyr	Ala	Gln 35	Pro	Pro	Leu	Gly	Arg 40	Leu	Arg	Phe	Lys 45	Lys	Pro	Gln	Ser
Leu	Thr 50	Lys	Trp	Ser	Asp	Ile 55	Trp	Asn	Ala	Thr 60	Lys	Tyr	Ala	Asn	Ser
Cys 65	Cys	Gln	Asn	Ile	Asp 70	Gln	Ser	Phe	Pro	Gly 75	Phe	His	Gly	Ser	Glu 80
Met	Trp	Asn	Pro	Asn 85	Thr	Asp	Leu	Ser	Glu 90	Asp	Cys	Leu	Tyr	Leu	Asn 95
Val	Trp	Ile	Pro 100	Ala	Pro	Lys	Pro	Lys 105	Asn	Ala	Thr 110	Val	Leu	Ile	Trp
Ile	Tyr	Gly 115	Gly	Gly	Phe	Gln	Thr 120	Gly	Thr	Ser	Ser 125	Leu	His	Val	Tyr
Asp	Gly 130	Lys	Phe	Leu	Ala	Arg 135	Val	Glu	Arg	Val 140	Ile	Val	Val	Ser	Met
Asn 145	Tyr	Arg	Val	Gly	Ala 150	Leu	Gly	Phe	Leu	Ala 155	Leu	Pro	Gly	Asn	Pro 160
Glu	Ala	Pro	Gly	Asn 165	Met	Gly	Leu	Phe	Asp 170	Gln	Gln	Leu	Ala	Leu	Gln 175
Trp	Val	Gln	Lys 180	Asn	Ile	Ala	Ala 185	Phe	Gly	Gly	Asn 190	Pro	Lys	Ser	Val
Thr	Leu	Phe 195	Gly	Glu	Ser	Ala	Gly 200	Ala	Ala	Ser	Val 205	Ser	Leu	His	Leu
Leu	Ser 210	Pro	Gly	Ser	His	Ser 215	Leu	Phe	Thr	Arg	Ala 220	Ile	Leu	Gln	Ser
Gly 225	Ser	Xaa	Asn	Ala 230	Pro	Trp	Ala	Val	Thr	Ser 235	Leu	Tyr	Glu	Ala	Arg 240
Asn	Arg	Thr	Leu	Asn 245	Leu	Ala	Lys	Leu	Thr 250	Gly	Cys	Ser	Arg	Glu	Asn 255
Glu	Thr	Glu	Ile 260	Ile	Lys	Cys	Leu	Arg 265	Asn	Lys	Asp	Pro	Gln	Glu	Ile 270
Leu	Leu	Asn 275	Glu	Ala	Phe	Val	Val 280	Pro	Tyr	Gly	Thr 285	Pro	Leu	Ser	Val
Asn	Phe 290	Gly	Pro	Thr	Val	Asp 295	Gly	Asp	Phe	Leu	Thr 300	Asp	Met	Pro	Asp
Ile 305	Leu	Leu	Glu	Leu	Gly 310	Gln	Phe	Lys	Lys	Thr 315	Gln	Ile	Leu	Val	Gly 320
Val	Asn	Lys	Asp	Glu 325	Gly	Thr	Ala	Phe	Leu	Val 330	Tyr	Gly	Ala	Pro	Gly 335
Phe	Ser	Lys	Asp 340	Asn	Asn	Ser	Ile	Ile 345	Thr	Arg	Lys	Glu	Phe	Gln	Glu
Gly	Leu	Lys 355	Ile	Phe	Phe	Pro	Gly 360	Val	Ser	Glu	Phe	Gly 365	Lys	Glu	Ser
Ile	Leu 370	Phe	His	Tyr	Thr	Asp 375	Trp	Val	Asp	Asp 380	Gln	Arg	Pro	Glu	Asn
Tyr 385	Arg	Glu	Ala	Leu	Gly 390	Asp	Val	Val	Gly	Asp 395	Tyr	Asn	Phe	Ile	Cys 400
Pro	Ala	Leu	Glu	Phe 405	Thr	Lys	Lys	Phe	Ser	Glu 410	Trp	Gly	Asn	Asn	Ala 415

Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Gln Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 125

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 125

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96

Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144

Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192

Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240

Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288

Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110	336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125	384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
ggt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008

Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340				345					350				
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355				360					365					
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385				390					395					400		
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
			405					410					415			
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
		420					425				430					
ggg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344
Gly	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
	435					440					445					
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
	450				455					460						
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465				470			475							480		
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
			485				490					495				
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
		500					505					510				
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515				520					525					
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	
	530				535						540					
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa	1680
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	

545		550		555		560								
ttt	aac	gat	tac	act	agc	aag	aaa	gaa	agt	tgt	gtg	ggt	ctc	1722
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu	
				565				570						

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<210> 126
<211> 574
<212> PRT
<213> Artificial Sequence
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<220>  
<223> synthetic butyrylcholinesterase variant

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<220>  
<221>VARIANT  
<222> 227  
<223> Xaa = Ala
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<400>	126														
Glu 1	Asp	Asp	Ile	Ile 5	Ile	Ala	Thr	Lys	Asn 10	Gly	Lys	Val	Arg	Gly 15	Met
Asn	Leu	Thr	Val 20	Phe	Gly	Gly	Thr	Val 25	Thr	Ala	Phe	Leu	Gly 30	Ile	Pro
Tyr	Ala	Gln 35	Pro	Pro	Leu	Gly	Arg 40	Leu	Arg	Phe	Lys 45	Lys	Pro	Gln	Ser
Leu	Thr 50	Lys	Trp	Ser	Asp	Ile 55	Trp	Asn	Ala	Thr	Lys 60	Tyr	Ala	Asn	Ser
Cys 65	Cys	Gln	Asn	Ile	Asp 70	Gln	Ser	Phe	Pro	Gly 75	Phe	His	Gly	Ser	Glu 80
Met	Trp	Asn	Pro	Asn 85	Thr	Asp	Leu	Ser	Glu 90	Asp	Cys	Leu	Tyr	Leu 95	Asn
Val	Trp	Ile	Pro 100	Ala	Pro	Lys	Pro	Lys 105	Asn	Ala	Thr	Val	Leu 110	Ile	Trp
Ile	Tyr	Gly 115	Gly	Gly	Phe	Gln	Thr 120	Gly	Thr	Ser	Ser	Leu 125	His	Val	Tyr
Asp	Gly 130	Lys	Phe	Leu	Ala	Arg 135	Val	Glu	Arg	Val	Ile 140	Val	Val	Ser	Met
Asn 145	Tyr	Arg	Val	Gly	Ala 150	Leu	Gly	Phe	Leu	Ala 155	Leu	Pro	Gly	Asn	Pro 160
Glu	Ala	Pro	Gly	Asn 165	Met	Gly	Leu	Phe	Asp 170	Gln	Gln	Leu	Ala 175	Leu	Gln
Trp	Val	Gln	Lys 180	Asn	Ile	Ala	Ala 185	Phe	Gly	Gly	Asn	Pro	Lys 190	Ser	Val
Thr	Leu	Phe 195	Gly	Glu	Ser	Ala	Gly 200	Ala	Ala	Ser	Val	Ser 205	Leu	His	Leu
Leu	Ser 210	Pro	Gly	Ser	His	Ser 215	Leu	Phe	Thr	Arg	Ala 220	Ile	Leu	Gln	Ser
Gly 225	Ser	Xaa	Asn	Ala	Pro 230	Trp	Ala	Val	Thr	Ser 235	Leu	Tyr	Glu	Ala	Arg 240
Asn	Arg	Thr	Leu	Asn 245	Leu	Ala	Lys	Leu	Thr 250	Gly	Cys	Ser	Arg	Glu 255	Asn
Glu	Thr	Glu	Ile 260	Ile	Lys	Cys	Leu	Arg 265	Asn	Lys	Asp	Pro	Gln 270	Glu	Ile
Leu	Leu	Asn 275	Glu	Ala	Phe	Val	Val 280	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp

290		295		300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly				
305		310		320
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly				
	325		330	335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu				
	340		345	350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser				
	355		360	365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn				
	370		375	380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys				
385		390		400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala				
	405		410	415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu				
	420		425	430
Gly Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu				
	435		440	445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser				
	450		455	460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro				
465		470		480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr				
	485		490	495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr				
	500		505	510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys				
	515		520	525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys				
	530		535	540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln				
545		550		560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu				
	565		570	

&lt;210&gt; 127

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 127

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
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Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser		
	35						40					45					
ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser		
	50					55					60						
tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu		
	65				70					75					80		
atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288	
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn		
				85					90					95			
gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp		
			100					105					110				
att	tat	ggg	ggg	ggg	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		
		115				120						125					
gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met		
	130					135					140						
aac	tat	agg	gtg	ggg	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro		
	145				150					155					160		
gag	gct	cca	ggg	aac	atg	ggg	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln		
				165					170					175			
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggg	gga	aat	cct	aaa	agt	gta	576	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val		
			180					185					190				
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195					200					205					
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
		210				215					220						
ggg	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
	225				230					235					240		
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggg	tgc	tct	aga	gag	aat	768	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		
				245					250					255			
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		

260	265	270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg ttt gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Phe Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495			1488



gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 128

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 128

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met.  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175

Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val		
			180					185					190				
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195					200					205					
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
	210					215					220						
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
225					230					235					240		
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		
				245					250					255			
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260						265				270				
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val		
	275							280					285				
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp		
	290					295					300						
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly		
305					310					315					320		
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly		
				325					330					335			
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu		
			340						345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser		
		355					360					365					
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn		
	370					375					380						
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys		
385					390					395					400		
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
				405					410					415			
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu		
		420						425					430				
Trp	Phe	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435					440					445					
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
	450					455						460					
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470					475					480		
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		
				485					490					495			
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr		
		500					505					510					
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys		
		515					520					525					
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys		
	530					535					540						
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
545					550					555					560		
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu				
				565					570								

&lt;210&gt; 129

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 129

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	

ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggc tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggc tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296

tgg ggg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta 1344  
 Trp Gly Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
           435                                  440                                  445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
           450                                  455                                  460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
           465                                  470                                  475                                  480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
                                   485                                  490                                  495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                                   500                                  505                                  510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
                                   515                                  520                                  525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
           530                                  535                                  540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
           545                                  550                                  555                                  560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                                   565                                  570

<210> 130

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221> VARIANT

<222> 227

<223> Xaa = Ala

<400> 130

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1                                  5                                  10                                  15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
                                   20                                  25                                  30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
           35                                  40                                  45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser

50						55						60					
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu		
65					70					75					80		
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn		
				85					90					95			
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp		
			100					105					110				
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		
		115					120					125					
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met		
	130					135					140						
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro		
145					150				155						160		
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln		
				165					170					175			
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val		
			180					185					190				
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195					200					205					
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
	210					215					220						
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
225				230					235					240			
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		
				245					250					255			
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260					265					270				
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val		
		275					280					285					
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp		
	290					295					300						
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly		
305					310					315					320		
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly		
				325					330					335			
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu		
			340					345					350				
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser		
		355					360					365					
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn		
	370					375					380						
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys		
385					390				395					400			
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
				405					410					415			
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu		
		420						425					430				
Trp	Gly	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435					440					445					
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
	450					455					460						
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470				475						480		
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		
				485					490					495			
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr		
			500					505					510				

Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
		515					520					525			
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys
	530					535					540				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln
545					550					555					560
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu		
			565					570							

$\langle 210 \rangle$  131

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS.

 $\langle 222 \rangle \quad (1) \dots (1722)$ 

<223> synthetic butyrylcholinesterase variant

<400> 131

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
20 25 30

tat	gca	cag	cca	cct	ctt	ggt	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35				40					45					

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
100 105 110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat 384  
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
115 120 125

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg 432  
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
130 135 140

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
ggt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152



Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn		
370						375					380						
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys		
385					390					395					400		
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248	
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
				405					410					415			
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu		
				420				425						430			
tgg	aag	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344	
Trp	Lys	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435					440					445					
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392	
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
		450				455					460						
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440	
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470					475					480		
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488	
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		
				485					490					495			
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr		
			500					505					510				
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584	
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys		
		515					520					525					
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632	
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys		
		530				535					540						
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa	1680	
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
545					550					555					560		
ttt	aac	gat	tac	act	agc	aag	aaa	gaa	agt	tgt	gtg	ggt	ctc			1722	
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu				
				565						570							

&lt;210&gt; 132

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 132

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
1.				5					10					15	
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120						125		
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
	195						200						205		
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230						235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
			325						330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys

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385          390          395          400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
          405          410          415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
          420          425          430
Trp Lys Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
          435          440          445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
          450          455          460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465          470          475          480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
          485          490          495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
          500          505          510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
          515          520          525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
          530          535          540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545          550          555          560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
          565          570

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&lt;210&gt; 133

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 133

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gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg      48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met
  1              5              10              15

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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc      96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
          20              25              30

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tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct      144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
          35              40              45

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ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct      192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
          50              55              60

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tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag      240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu
          65              70              75              80

```

atg tgg aac cca aac act gac ctc agt gaa gac/tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960

Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggg	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggg	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
tac	cgt	gag	gcc	ttg	ggg	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
tgg	ctg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggg	tta	1344
Trp	Leu	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
		450				455					460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490				495			
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
			500					505					510			
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	

530

535

540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

&lt;210&gt; 134

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 134

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile

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<210> 135
<211> 1722
<212> DNA
<213> Artificial Sequence
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<220>  
<221> CDS  
<222> (1) ... (1722)
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<223> synthetic butyrylcholinesterase variant

<400> 135  
gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg  
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768



Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
			275				280					285				
aac	ttt	ggt	ccg	acc	gtg	gat	ggt	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405				410						415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
tgg	aat	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344
Trp	Asn	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
		450				455					460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	

465	470	475	480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act				1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr				
	485	490	495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg				1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr				
	500	505	510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa				1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys				
	515	520	525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa				1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys				
	530	535	540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa				1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln				
	545	550	555	560
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc				1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu				
	565	570		

&lt;210&gt; 136

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 136

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met				
1	5	10	15	
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro				
	20	25	30	
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser				
	35	40	45	
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser				
	50	55	60	
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu				
	65	70	75	80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn				
	85	90	95	
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp				
	100	105	110	
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr				
	115	120	125	
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met				

130	135	140
Asn Tyr Arg Val Gly Ala	Leu Gly Phe Leu Ala	Leu Pro Gly Asn Pro
145	150	155
Glu Ala Pro Gly Asn Met Gly	Leu Phe Asp Gln Gln	Leu Ala Leu Gln
165	170	175
Trp Val Gln Lys Asn Ile Ala	Ala Phe Gly Gly Asn Pro	Lys Ser Val
180	185	190
Thr Leu Phe Gly Glu Ser Ala	Gly Ala Ala Ser Val	Ser Leu His Leu
195	200	205
Leu Ser Pro Gly Ser His Ser	Leu Phe Thr Arg Ala	Ile Leu Gln Ser
210	215	220
Gly Ser Xaa Asn Ala Pro Trp	Ala Val Thr Ser Leu	Tyr Glu Ala Arg
225	230	235
Asn Arg Thr Leu Asn Leu Ala	Lys Leu Thr Gly Cys Ser	Arg Glu Asn
245	250	255
Glu Thr Glu Ile Ile Lys Cys	Leu Arg Asn Lys Asp Pro	Gln Glu Ile
260	265	270
Leu Leu Asn Glu Ala Phe Val	Val Pro Tyr Gly Thr Pro	Leu Ser Val
275	280	285
Asn Phe Gly Pro Thr Val Asp	Gly Asp Phe Leu Thr Asp	Met Pro Asp
290	295	300
Ile Leu Leu Glu Leu Gly Gln	Phe Lys Lys Thr Gln	Ile Leu Val Gly
305	310	315
Val Asn Lys Asp Glu Gly Thr	Ala Phe Leu Val Tyr Gly	Ala Pro Gly
325	330	335
Phe Ser Lys Asp Asn Asn Ser	Ile Ile Thr Arg Lys Glu	Phe Gln Glu
340	345	350
Gly Leu Lys Ile Phe Phe Pro	Gly Val Ser Glu Phe Gly	Lys Glu Ser
355	360	365
Ile Leu Phe His Tyr Thr Asp	Trp Val Asp Asp Gln Arg	Pro Glu Asn
370	375	380
Tyr Arg Glu Ala Leu Gly Asp	Val Val Gly Asp Tyr Asn	Phe Ile Cys
385	390	395
Pro Ala Leu Glu Phe Thr Lys	Lys Phe Ser Glu Trp Gly	Asn Asn Ala
405	410	415
Phe Phe Tyr Tyr Phe Glu His	Arg Ser Ser Lys Leu Pro	Trp Pro Glu
420	425	430
Trp Asn Gly Val Met His Gly	Tyr Glu Ile Glu Phe Val	Phe Gly Leu
435	440	445
Pro Leu Glu Arg Arg Asp Asn	Tyr Thr Lys Ala Glu Glu	Ile Leu Ser
450	455	460
Arg Ser Ile Val Lys Arg Trp	Ala Asn Phe Ala Lys Tyr	Gly Asn Pro
465	470	475
Asn Glu Thr Gln Asn Asn Ser	Thr Ser Trp Pro Val Phe	Lys Ser Thr
485	490	495
Glu Gln Lys Tyr Leu Thr Leu	Asn Thr Glu Ser Thr Arg	Ile Met Thr
500	505	510
Lys Leu Arg Ala Gln Gln Cys	Arg Phe Trp Thr Ser Phe	Phe Pro Lys
515	520	525
Val Leu Glu Met Thr Gly Asn	Ile Asp Glu Ala Glu Trp	Glu Trp Lys
530	535	540
Ala Gly Phe His Arg Trp Asn	Asn Tyr Met Met Asp Trp	Lys Asn Gln
545	550	555
Phe Asn Asp Tyr Thr Ser Lys	Lys Glu Ser Cys Val Gly	Leu
565	570	

<211> 1722  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 137

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	

tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	

180	185	190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205			624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248

ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa 1296  
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
420 425 430

tgg tcg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta 1344  
Trp Ser Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
435 440 445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
450 455 460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
565 570

<210> 138

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221> VARIANT

<222> 227

<223> Xaa = Ala

<400> 138

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
1 5 10 15

Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430
Trp	Ser	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	450	455	460
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro			

465		470		475		480									
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr
				485					490					495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr
			500					505					510		
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
		515					520					525			
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys
	530					535					540				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln
545					550				555					560	
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu		
			565					570							

&lt;210&gt; 139

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 139

gaa	gat	gac	atc	ata	att	gca	aca	aag	aat	gga	aaa	gtc	aga	ggg	atg	48
Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	
1				5					10					15		

aac	ttg	aca	gtt	ttt	ggt	ggc	acg	gta	aca	gcc	ttt	ctt	gga	att	ccc	96
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	
			20					25					30			

tat	gca	cag	cca	cct	ctt	ggt	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35				40						45				

ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50				55				60							

tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65				70				75						80		

atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
			85					90						95		

gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			

att	tat	ggt	ggt	ggt	ttt	caa	act	gga	aca	tca	tct	tta	cat	ggt	tat	384
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				



gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056

ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg tgg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Trp Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465 470 475 480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act	1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr	
485 490 495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg	1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr	
500 505 510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa	1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys	
515 520 525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa	1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys	
530 535 540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa	1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln	
545 550 555 560	
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc	1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu	
565 570	

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 140

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350	

Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Trp Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 141

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 141

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu 65 70 75 80	240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95	288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110	336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125	384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864

aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggc tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg tgt gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Cys Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510	1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa	1584

Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 142

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 142

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220

Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365	
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395	400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430	
Trp	Met	Cys	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445	
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	450	455	460	
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	465	470	475	480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	485	490	495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	500	505	510	
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	515	520	525	
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	530	535	540	
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	545	550	555	560
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu			565	570		

&lt;210&gt; 143

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 143



gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met 1 5 10 15	48
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro 20 25 30	96
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser 35 40 45	144
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser 50 55 60	192
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu 65 70 75 80	240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95	288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110	336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125	384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720

Gly 225	Ser	Xaa	Asn	Ala	Pro 230	Trp	Ala	Val	Thr	Ser 235	Leu	Tyr	Glu	Ala	Arg 240	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggt	tgc	tct	aga	gag	aat	768
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
aac	ttt	ggt	ccg	acc	gtg	gat	ggt	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315				320		
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330				335			
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390				395					400		
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
tgg	atg	gga	gtg	ggg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344
Trp	Met	Gly	Val	Gly	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	

450	455	460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca			1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro			
465	470	475	480
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act			1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr			
485	490	495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg			1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr			
500	505	510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa			1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys			
515	520	525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa			1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys			
530	535	540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa			1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln			
545	550	555	560
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc			1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu			
565	570		

&lt;210&gt; 144

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 144

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met			
1	5	10	15
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro			
20	25	30	
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser			
35	40	45	
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser			
50	55	60	
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu			
65	70	75	80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn			
85	90	95	
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp			

			100					105				110			
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170						175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225					230					235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
			275				280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
				405					410				415		
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
			420					425					430		
Trp	Met	Gly	Val	Gly	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
		435					440					445			
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser
	450														

Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
565 570

<210> 145

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 145

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
100 105 110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat 384  
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
115 120 125

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg 432  
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
130 135 140

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct 480  
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
145 150 155 160

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag 528  
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln



cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc 1248  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
                     405                    410                    415

ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa 1296  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
                     420                    425                    430

tgg atg gga gtg att cat ggc tat gaa att gaa ttt gtc ttt ggt tta 1344  
 Trp Met Gly Val Ile His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
                     435                    440                    445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
                     450                    455                    460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
                     465                    470                    475                    480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
                     485                    490                    495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                     500                    505                    510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
                     515                    520                    525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
                     530                    535                    540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
                     545                    550                    555                    560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                     565                    570

<210> 146

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 146

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
1				5					10					15	
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
	115					120						125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225					230					235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
		275						280				285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
				405					410					415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
			420					425					430		



Trp Met Gly Val Ile His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 147

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 147

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336

Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp		
			100					105					110				
att	tat	ggt	ggt	ggt	ttt	caa	act	gga	aca	tca	tct	tta	cat	ggt	tat	384	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		
		115					120					125					
gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	ggt	att	gta	gtg	tca	atg	432	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met		
	130					135					140						
aac	tat	agg	gtg	ggt	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro		
145					150					155					160		
gag	gct	cca	ggg	aac	atg	ggt	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln		
				165					170					175			
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggt	gga	aat	cct	aaa	agt	gta	576	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val		
			180					185						190			
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195					200					205					
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
	210					215					220						
ggt	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
225					230					235					240		
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggt	tgc	tct	aga	gag	aat	768	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		
				245					250					255			
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260					265					270				
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val		
		275					280					285					
aac	ttt	ggt	ccg	acc	gtg	gat	ggt	gat	ttt	ctc	act	gac	atg	cca	gac	912	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp		
	290					295					300						
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly		
305					310					315					320		
ggt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008	
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly		

325	330	335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggc tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat acg tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Thr Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495			1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510			1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525			1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540			1632
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln 545 550 555 560			1680

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                   565                                  570

1722

<210> 148  
 <211> 574  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic butyrylcholinesterase variant

<220>  
 <221>VARIANT  
 <222> 227  
 <223> Xaa = Ala

<400> 148  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
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 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
                   20                  25                  30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
                   35                  40                  45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
                   50                  55                  60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
   65                  70                  75                  80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
                   85                  90                  95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
                   100                  105                  110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
                   115                  120                  125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
                   130                  135                  140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
   145                  150                  155                  160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
                   165                  170                  175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
                   180                  185                  190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
                   195                  200                  205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
                   210                  215                  220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
   225                  230                  235                  240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
                   245                  250                  255  
 Glu Thr Glu Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
                   260                  265                  270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val  
                   275                  280                  285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
                   290                  295                  300

Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly  
 325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350  
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Thr Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 149

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 149

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	

35	40	45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser 50 55 60			192
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu 65 70 75 80			240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95			288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110			336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125			384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140			432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160			480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175			528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190			576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205			624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816

ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc gct gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Ala Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                   500                                  505                                  510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
                   515                                  520                                  525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
                   530                                  535                                  540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
                   545                                  550                                  555                                  560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                                   565                                  570

<210> 150

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221> VARIANT

<222> 227

<223> Xaa = Ala

<400> 150

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1                  5                  10                  15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
                   20                  25                  30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
                   35                  40                  45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
                   50                  55                  60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65                  70                  75                  80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
                   85                  90                  95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
                   100                  105                  110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
                   115                  120                  125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
                   130                  135                  140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145                  150                  155                  160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
                   165                  170                  175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val



			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
		210				215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225					230					235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
			275				280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
		290				295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
		370				375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
				405					410					415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
			420					425					430		
Trp	Met	Gly	Val	Met	His	Gly	Ala	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
		435					440					445			
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser
		450				455					460				
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro
465					470					475					480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr
				485					490					495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr
			500					505					510		
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
		515													

<210> 151

<211> 1722

<212> DNA

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<221> CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 151

gaa	gat	gac	atc	ata	att	gca	aca	aag	aat	gga	aaa	gtc	aga	ggg	atg	48
Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	
1				5					10					15		

aac	ttg	aca	gtt	ttt	ggt	ggc	acg	gta	aca	gcc	ttt	ctt	gga	att	ccc	96
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	
			20					25					30			

tat	gca	cag	cca	cct	ctt	ggt	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35					40					45				

ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50					55					60					

tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65				70						75					80	

atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		

gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			

att	tat	ggt	ggt	ggt	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				

gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					

aac	tat	agg	gtg	ggt	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	

gag	gct	cca	ggg	aac	atg	ggt	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
			165						170				175			

tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggt	gga	aat	cct	aaa	agt	gta	576
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
		180						185					190			

act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				

ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggg tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc gag gaa att gaa ttt gtc ttt ggt tta	1344

Trp Met Gly Val Met His Gly Glu Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465 470 475 480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act	1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr	
485 490 495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg	1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr	
500 505 510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa	1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys	
515 520 525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa	1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys	
530 535 540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa	1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln	
545 550 555 560	
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc	1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu	
565 570	

&lt;210&gt; 152

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 152

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	

50		55		60
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu				
65	70	75	80	
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn				
	85	90	95	
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp				
	100	105	110	
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr				
	115	120	125	
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met				
	130	135	140	
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro				
145	150	155	160	
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln				
	165	170	175	
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val				
	180	185	190	
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu				
	195	200	205	
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser				
	210	215	220	
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg				
225	230	235	240	
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn				
	245	250	255	
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile				
	260	265	270	
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val				
	275	280	285	
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp				
	290	295	300	
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly				
305	310	315	320	
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly				
	325	330	335	
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu				
	340	345	350	
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser				
	355	360	365	
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn				
	370	375	380	
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys				
385	390	395	400	
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala				
	405	410	415	
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu				
	420	425	430	
Trp Met Gly Val Met His Gly Glu Ile Glu Phe Val Phe Gly Leu				
	435	440	445	
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser				
	450	455	460	
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro				
465	470	475	480	
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr				
	485	490	495	
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr				
	500	505	510	

Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
		515					520					525			
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys
	530					535					540				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln
545					550					555					560
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu		
				565					570						

<210> 153

<211> 1722

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (1722)$ 

<223> synthetic butyrylcholinesterase variant

<400> 153

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
1 5 10 15

aac ttg aca gtt. ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
100 105 110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat 384  
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
115 120 125

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg 432  
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
130 135 140

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggg tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
ggt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152

Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn		
370						375					380						
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc		1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys		
385					390					395					400		
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc		1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
				405					410						415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa		1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu		
			420					425						430			
tgg	atg	gga	gtg	atg	cat	ggc	ttt	gaa	att	gaa	ttt	gtc	ttt	ggt	tta		1344
Trp	Met	Gly	Val	Met	His	Gly	Phe	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
	435						440					445					
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt		1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
	450					455					460						
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca		1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470					475					480		
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act		1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		
				485					490						495		
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg		1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr		
			500					505					510				
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa		1584
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys		
		515					520					525					
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa		1632
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys		
	530					535					540						
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa		1680
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
545					550					555					560		
ttt	aac	gat	tac	act	agc	aag	aaa	gaa	agt	tgt	gtg	ggt	ctc				1722
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu				
				565						570							

&lt;210&gt; 154

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;



<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 154

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
1				5					10					15	
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200						205		
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225					230					235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys

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385          390          395          400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
          405          410          415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
          420          425          430
Trp Met Gly Val Met His Gly Phe Glu Ile Glu Phe Val Phe Gly Leu
          435          440          445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
          450          455          460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465          470          475          480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
          485          490          495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
          500          505          510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
          515          520          525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
          530          535          540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545          550          555          560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
          565          570

```

<210> 155

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 155

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gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg      48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met
 1              5              10              15

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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc      96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
          20              25              30

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tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct      144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
          35              40              45

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ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct      192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
          50              55              60

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tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag      240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu
          65              70              75              80

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atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggg tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960

Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggg	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
				340				345					350			
ggg	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggg	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
tgg	atg	gga	gtg	atg	cat	ggc	ggg	gaa	att	gaa	ttt	gtc	ttt	ggg	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	Gly	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
		450				455					460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490					495		
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
			500					505					510			
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	

530

535

540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt .ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

&lt;210&gt; 156

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 156

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile

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                260                265                270
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val
                275                280                285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp
                290                295                300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly
305                310                315                320
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly
                325                330                335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
                340                345                350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
                355                360                365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
370                375                380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385                390                395                400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
                405                410                415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
                420                425                430
Trp Met Gly Val Met His Gly Gly Glu Ile Glu Phe Val Phe Gly Leu
                435                440                445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
450                455                460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465                470                475                480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
                485                490                495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
500                505                510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
515                520                525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
530                535                540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545                550                555                560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
                565                570

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&lt;210&gt; 157

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 157

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gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met
  1             5             10             15

```

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro 20 25 30	96
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser 35 40 45	144
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser 50 55 60	192
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu 65 70 75 80	240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95	288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110	336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125	384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768

Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
aac	ttt	ggt	ccg	acc	gtg	gat	ggt	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305				310						315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
			325					330					335			
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385				390					395						400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405				410					415			
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
		420						425				430				
tgg	atg	gga	gtg	atg	cat	ggc	cat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	His	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435				440						445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
		450				455					460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	



465	470	475	480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act				1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr				
485		490	495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg				1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr				
500		505	510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa				1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys				
515		520	525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa				1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys				
530		535	540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa				1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln				
545	550	555	560	
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc				1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu				
565		570		

&lt;210&gt; 158

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 158

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met				
1	5	10	15	
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro				
20	25	30		
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser				
35	40	45		
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser				
50	55	60		
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu				
65	70	75	80	
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn				
85	90	95		
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp				
100	105	110		

Ile	Tyr	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115				120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Met
	130					135					140			
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Pro
145					150					155				160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Gln
				165					170					175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Val
			180					185					190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	Leu
		195					200					205		
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Ser
	210					215					220			
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Arg
225					230					235				240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Asn
				245					250					255
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Ile
			260					265					270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Val
			275				280					285		
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Asp
	290					295					300			
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Gly
305					310					315				320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Gly
				325					330					335
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Glu
			340					345					350	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Ser
		355					360					365		
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Asn
	370					375					380			
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Cys
385					390					395				400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Ala
				405					410					415
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Glu
			420					425					430	
Trp	Met	Gly	Val	Met	His	Gly	His	Glu	Ile	Glu	Phe	Val	Phe	Leu
		435				440						445		
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Ser
	450				455						460			
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Pro
465					470					475				480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp					

565

570

&lt;210&gt; 159

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 159

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
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Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
				165					170					175		
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggg	gga	aat	cct	aaa	agt	gta	576
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
	210					215					220					
ggg	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggg	tgc	tct	aga	gag	aat	768
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ttg	tca	gta	864
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
aac	ttt	ggg	ccg	acc	gtg	gat	ggg	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggg	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tat	ggg	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330				335			
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggg	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
tac	cgt	gag	gcc	ttg	ggg	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	

385	390	395	400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc				1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala				
405		410	415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa				1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu				
420		425	430	
tgg atg gga gtg atg cat ggc ttg gaa att gaa ttt gtc ttt ggt tta				1344
Trp Met Gly Val Met His Gly Leu Glu Ile Glu Phe Val Phe Gly Leu				
435		440	445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt				1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser				
450		455	460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca				1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro				
465		470	475	480
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act				1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr				
485		490	495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg				1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr				
500		505	510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa				1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys				
515		520	525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa				1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys				
530		535	540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa				1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln				
545		550	555	560
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc				1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu				
565		570		

&lt;210&gt; 160

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 160

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365	
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395	400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430	

Trp Met Gly Val Met His Gly Leu Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 161

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 161

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp

100	105	110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125			384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140			432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160			480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175			528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190			576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205			624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008



ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggc tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc atg gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Met Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510	1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525	1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540	1632
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln 545 550 555 560	1680

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

1722

&lt;210&gt; 162

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 162

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly

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305          310          315          320
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly
          325          330          335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
          340          345          350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
          355          360          365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
          370          375          380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385          390          395          400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
          405          410          415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
          420          425          430
Trp Met Gly Val Met His Gly Met Glu Ile Glu Phe Val Phe Gly Leu
          435          440          445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
          450          455          460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465          470          475          480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
          485          490          495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
          500          505          510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
          515          520          525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
          530          535          540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545          550          555          560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
          565          570

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&lt;210&gt; 163

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 163

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gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg      48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met
1          5          10          15

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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc      96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
          20          25          30

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tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct      144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser

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35	40	45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser 50 55 60			192
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu 65 70 75 80			240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95			288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110			336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125			384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140			432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160			480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175			528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190			576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205			624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816

ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc	1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	
325 330 335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	
340 345 350	
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc	1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	
355 360 365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc aat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Asn Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465 470 475 480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act	1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr	
485 490 495	

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 164

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 164

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175

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<210> 165
<211> 1722
<212> DNA
<213> Artificial Sequence
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### <213> Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 165

gaa	gat	gac	atc	ata	att	gca	aca	aag	aat	gga	aaa	gtc	aga	ggg	atg	48
Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	
1				5					10					15		

aac	ttg	aca	ggt	ttt	ggt	ggc	acg	gta	aca	gcc	ttt	ctt	gga	att	ccc	96
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	
			20					25					30			

tat	gca	cag	cca	cct	ctt	ggt	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35					40					45				

ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50					55					60					

tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65					70					75					80	

atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		

gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			

att	tat	ggt	ggt	ggt	ttt	caa	act	gga	aca	tca	tct	tta	cat	ggt	tat	384
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				

gat	ggc	aag	ttt	ctg	gct	cgg	ggt	gaa	aga	ggt	att	gta	gtg	tca	atg	432
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					

aac	tat	agg	gtg	ggt	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	

gag	gct	cca	ggg	aac	atg	ggt	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
			165						170					175		

tgg	ggt	caa	aaa	aat	ata	gca	gcc	ttt	ggt	gga	aat	cct	aaa	agt	gta	576
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			

act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	ggt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	



195	200	205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296

tgg atg gga gtg atg cat ggc cag gaa att gaa ttt gtc ttt ggt tta 1344  
 Trp Met Gly Val Met His Gly Gln Glu Ile Glu Phe Val Phe Gly Leu  
           435                          440                          445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
           450                          455                          460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
           465                          470                          475                          480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
                                   485                          490                          495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                           500                          505                          510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
           515                          520                          525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
           530                          535                          540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
           545                          550                          555                          560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                                   565                          570

<210> 166

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221> VARIANT

<222> 227

<223> Xaa = Ala

<400> 166

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
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 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
           20                  25                  30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser

		35					40					45				
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50					55					60					
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65					70					75					80	
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115				120						125				
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
				165					170					175		
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
	210					215					220					
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
Glu	Thr	Glu	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260				265					270				
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395						

Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                   500                  505                  510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
                   515                  520                  525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
                   530                  535                  540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
                   545                  550                  555                  560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                   565                  570

<210> 167

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 167

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
   1                  5                  10                  15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
                   20                  25                  30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
                   35                  40                  45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
                   50                  55                  60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
                   65                  70                  75                  80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
                   85                  90                  95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
                   100                  105                  110

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat 384  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
                   115                  120                  125

gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg 432  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met

130	135	140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160			480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175			528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190			576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205			624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggg tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser			1104

355	360	365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc agg gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Arg Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495			1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510			1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525			1584
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys 530 535 540			1632
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln 545 550 555 560			1680
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu 565 570			1722

&lt;210&gt; 168

&lt;211&gt; 574

&lt;212&gt; PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 168

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365	

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Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
 370          375          380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385          390          395          400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
          405          410          415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
          420          425          430
Trp Met Gly Val Met His Gly Arg Glu Ile Glu Phe Val Phe Gly Leu
          435          440          445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
          450          455          460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465          470          475          480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
          485          490          495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
          500          505          510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
          515          520          525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
          530          535          540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545          550          555          560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
          565          570

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<210> 169

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 169

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gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg      48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met
 1          5          10          15

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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc      96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
          20          25          30

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tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct      144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
          35          40          45

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ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct      192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
          50          55          60

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tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag      240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu

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65	70	75	80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat				288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	85	90	95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg				336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	100	105	110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat				384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	115	120	125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg				432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	130	135	140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct				480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	145	150	155	160
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag				528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	165	170	175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta				576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	180	185	190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg				624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	195	200	205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt				672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	210	215	220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg				720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	225	230	235	240
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat				768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	245	250	255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att				816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	260	265	270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta				864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	275	280	285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac				912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	290	295	300	

ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296
tgg atg gga gtg atg cat ggc tct gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Ser Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 500 505 510	1536
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys 515 520 525	1584

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 170

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 170

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn

				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
			325						330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
				405					410					415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
			420					425					430		
Trp	Met	Gly	Val	Met	His	Gly	Ser	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
		435					440					445			
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser
	450					455					460				
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro
465					470					475					480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr
				485					490					495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr
			500					505					510		
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
		515					520					525			
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys
	530					535					540				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln
545					550					555					560
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu		
				565					570						

<210> 171

<211> 1722

<212> DNA

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (1722)$ 

<223> synthetic butyrylcholinesterase variant

<400> 171

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg  
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	

225	230	235	240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat				768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	245	250	255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att				816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	260	265	270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta				864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val	275	280	285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac				912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	290	295	300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt				960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	305	310	315	320
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc				1008
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly	325	330	335	
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa				1056
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu	340	345	350	
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc				1104
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser	355	360	365	
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac				1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	370	375	380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc				1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys	385	390	395	400
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc				1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	405	410	415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa				1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	420	425	430	
tgg atg gga gtg atg cat ggc act gaa att gaa ttt gtc ttt ggt tta				1344
Trp Met Gly Val Met His Gly Thr Glu Ile Glu Phe Val Phe Gly Leu	435	440	445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt				1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	450	455	460	

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 172

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 172

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110

Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255
Glu	Thr	Glu	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		260	265	270
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	275	280	285
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430
Trp	Met	Gly	Val	Met	His	Gly	Thr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	450	455	460
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	465	470	475
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	485	490	495
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	500	505	510
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	515	520	525
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	530	535	540
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	545	550	555
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu					



565

570

&lt;210&gt; 173

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 173

gaa	gat	gac	atc	ata	att	gca	aca	aag	aat	gga	aaa	gtc	aga	ggg	atg	48
Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	
1			5					10						15		

aac	ttg	aca	gtt	ttt	ggt	ggc	acg	gta	aca	gcc	ttt	ctt	gga	att	ccc	96
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	
			20				25						30			

tat	gca	cag	cca	cct	ctt	ggt	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35					40					45				

ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50					55					60					

tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	cat	gga	tca	gag	240
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65				70				75							80	

atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
			85					90						95		

gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			

att	tat	ggt	ggt	ggt	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				

gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					

aac	tat	agg	gtg	ggt	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	

gag	gct	cca	ggg	aac	atg	ggt	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
			165					170						175		

tggtgttcaa	aaataat	atagcagcc	tttggtgga	aatcctaaa	agtgta	576	
TrpValGln	LysAsnIle	AlaAlaPhe	GlyGlyGly	AsnProLys	SerVal		
	180		185		190		
actctcttt	ggagaaagt	gcagga	gcagcttca	gttagcctg	catttg	624	
ThrLeuPhe	GlyGluSer	AlaGlyAla	AlaAlaSer	ValSerLeu	HisLeu		
	195		200		205		
ctttctcct	ggagagcat	tcatctgttg	ttctaccaga	gccattctg	caaatg	672	
LeuSerPro	GlySerHis	SerSerLeu	PheThrArg	AlaAlaIle	LeuGlnSer		
	210		215		220		
gggtccgck	aatgctcct	tgggcgtgta	acatctctt	tattaga	gctagg	720	
GlySerXaa	AsnAlaPro	TrpAlaVal	ThrSerLeu	TyrGluAla	Arg		
	225		230		235	240	
aacagaacg	ttgaactta	gctaaattg	actggttgc	tctaga	gagaaat	768	
AsnArgThr	LeuAsnLeu	AlaLysLeu	ThrGlyCys	SerArgGlu	Asn		
	245		250		255		
gagactgaa	ataatc	aagtgtctt	agaaataaa	gatccc	caagaaatt	816	
GluThrGlu	IleIleLys	CysLeuArg	AsnLysAsp	ProGlnGlu	Ile		
	260		265		270		
cttctgaat	gaagcattt	gttgctccc	tattgggact	cctttgtca	gtatg	864	
LeuLeuAsn	GluAlaPhe	ValValPro	TyrGlyThr	ProLeuSer	Val		
	275		280		285		
aactttggt	ccgaccgtg	gatggtgat	tttctcact	gacatgcca	gac	912	
AsnPheGly	ProThrVal	AspGlyAsp	PheLeuThr	AspMetPro	Asp		
	290		295		300		
atattactt	gaacttgga	caatttt	aaaacc	cagattttg	gtgggt	960	
IleLeuLeu	GluLeuGly	GlnPheLys	LysThrGln	IleLeuVal	Gly		
	305		310		315	320	
gttaataaa	gatgaaggga	acagctttt	ttagcttat	ggtgctcct	ggc	1008	
ValAsnLys	AspGluGly	ThrAlaPhe	LeuValTyr	GlyAlaPro	Gly		
	325		330		335		
ttcagcaaa	gatgaacaa	atagtagt	atcataact	agaaa	gaatttcag	gaa	1056
PheSerLys	AspAsnAsn	SerIleIle	ThrArgLys	GluPheGln	Glu		
	340		345		350		
gggttataaa	ataatttt	tttcca	ggagtgtg	agtgagt	tttggga	aaggaatcc	1104
GlyLeuLys	IlePhePhe	ProGlyVal	SerGluPhe	GlyLysGlu	Ser		
	355		360		365		
atccttttt	catctac	acagact	tggtgta	gatgat	cagaga	cctgaatcc	1152
IleLeuPhe	HisTyrThr	AspThrAsp	TrpValAsp	AspGlnArg	ProGluAsn		
	370		375		380		
tactcgtag	gaggcc	ttgggtgat	gttggtggg	gattatt	aatttc	atatgc	1200
TyrArgGlu	AlaLeuGly	AspValVal	GlyGlyGly	AspTyrAsn	PheIleCys		
	385		390		395	400	

cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc 1248  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
                   405                  410                  415

ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa 1296  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
                   420                  425                  430

tgg atg gga gtg atg cat ggc tat act att gaa ttt gtc ttt ggt tta 1344  
 Trp Met Gly Val Met His Gly Tyr Thr Ile Glu Phe Val Phe Gly Leu  
                   435                  440                  445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
                   450                  455                  460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
                   465                  470                  475                  480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
                   485                  490                  495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                   500                  505                  510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
                   515                  520                  525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
                   530                  535                  540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
                   545                  550                  555                  560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                   565                  570

<210> 174

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221> VARIANT

<222> 227

<223> Xaa = Ala

&lt;400&gt; 174

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
1				5					10					15	
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120						125		
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225					230					235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
			325						330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
				405					410					415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
			420					425					430		
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Thr	Ile	Glu	Phe	Val	Phe	Gly	Leu
		435					440					445			

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Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
  450                      455                      460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
  465                      470                      475                      480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
                      485                      490                      495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
                      500                      505                      510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
                      515                      520                      525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
                      530                      535                      540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
  545                      550                      555                      560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
                      565                      570

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&lt;210&gt; 175

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 175

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gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg      48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met
  1                      5                      10                      15

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```

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc      96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
                      20                      25                      30

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```

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct      144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
                      35                      40                      45

```

```

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct      192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
                      50                      55                      60

```

```

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag      240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu
  65                      70                      75                      80

```

```

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat      288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn
                      85                      90                      95

```

```

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg      336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp
                      100                      105                      110

```

att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125	384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa	1056

Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
		370				375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	ctg	gaa	ttt	gtc	ttt	ggt	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Leu	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
		450				455					460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470				475						480	
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490				495			
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
			500					505					510			
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	
		530				535					540					
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa	1680
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	
545					550					555					560	
ttt	aac	gat	tac	act	agc	aag	aaa	gaa	agt	tgt	gtg	ggt	ctc			1722
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu			

565

570

<210> 176  
 <211> 574  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic butyrylcholinesterase variant

<220>  
 <221>VARIANT  
 <222> 227  
 <223> Xaa = Ala

<400> 176  
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 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320



Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly  
 325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350  
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Leu Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 177

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 177

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser 50 55 60	192
tgc tgt cag aag ata gat caa agt ttt cca ggc ttc ttt gga tca gag Cys Cys Gln Lys Ile Asp Gln Ser Phe Pro Gly Phe Phe Gly Ser Glu 65 70 75 80	240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95	288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110	336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125	384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140	432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act aat ttg tca gta	864

Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Asn	Leu	Ser	Val	
		275					280					285				
aac	ttt	ggg	ccg	acc	gtg	gat	ggg	gat	ttt	ctc	act	gac	atg	cca	gac	912
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295				300						
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggg	960
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gcg	tat	ggg	gct	cct	ggc	1008
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Ala	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggg	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
tac	cgt	gag	gcc	ttg	ggg	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggg	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
		450				455					460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490					495		
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	

500	505	510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa			1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys			
515	520	525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa			1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys			
530	535	540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa			1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln			
545	550	555	560
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc			1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu			
565	570		

&lt;210&gt; 178

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 178

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met			
1	5	10	15
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro			
20	25	30	
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser			
35	40	45	
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser			
50	55	60	
Cys Cys Gln Lys Ile Asp Gln Ser Phe Pro Gly Phe Phe Gly Ser Glu			
65	70	75	80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn			
85	90	95	
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp			
100	105	110	
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr			
115	120	125	
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met			
130	135	140	
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro			
145	150	155	160
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln			
165	170	175	
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val			
180	185	190	
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu			

195	200	205
Leu Ser Pro Gly Ser His	Ser Leu Phe Thr Arg	Ala Ile Leu Gln Ser
210	215	220
Gly Ser Xaa Asn Ala Pro	Trp Ala Val Thr Ser	Leu Tyr Glu Ala Arg
225	230	235
Asn Arg Thr Leu Asn Leu	Ala Lys Leu Thr Gly	Cys Ser Arg Glu Asn
245	250	255
Glu Thr Glu Ile Ile Lys	Cys Leu Arg Asn Lys	Asp Pro Gln Glu Ile
260	265	270
Leu Leu Asn Glu Ala Phe	Val Val Pro Tyr Gly	Thr Asn Leu Ser Val
275	280	285
Asn Phe Gly Pro Thr Val	Asp Gly Asp Phe Leu	Thr Asp Met Pro Asp
290	295	300
Ile Leu Leu Glu Leu Gly	Gln Phe Lys Lys Thr	Gln Ile Leu Val Gly
305	310	315
Val Asn Lys Asp Glu Gly	Thr Ala Phe Leu Ala	Tyr Gly Ala Pro Gly
325	330	335
Phe Ser Lys Asp Asn Asn	Ser Ile Ile Thr Arg	Lys Glu Phe Gln Glu
340	345	350
Gly Leu Lys Ile Phe Phe	Pro Gly Val Ser Glu	Phe Gly Lys Glu Ser
355	360	365
Ile Leu Phe His Tyr Thr	Asp Trp Val Asp Asp	Gln Arg Pro Glu Asn
370	375	380
Tyr Arg Glu Ala Leu Gly	Asp Val Val Gly Asp	Tyr Asn Phe Ile Cys
385	390	395
Pro Ala Leu Glu Phe Thr	Lys Lys Phe Ser Glu	Trp Gly Asn Asn Ala
405	410	415
Phe Phe Tyr Tyr Phe Glu	His Arg Ser Ser Lys	Leu Pro Trp Pro Glu
420	425	430
Trp Met Gly Val Met His	Gly Tyr Glu Ile Glu	Phe Val Phe Gly Leu
435	440	445
Pro Leu Glu Arg Arg Asp	Asn Tyr Thr Lys Ala	Glu Glu Ile Leu Ser
450	455	460
Arg Ser Ile Val Lys Arg	Trp Ala Asn Phe Ala	Lys Tyr Gly Asn Pro
465	470	475
Asn Glu Thr Gln Asn Asn	Ser Thr Ser Trp Pro	Val Phe Lys Ser Thr
485	490	495
Glu Gln Lys Tyr Leu Thr	Leu Asn Thr Glu Ser	Thr Arg Ile Met Thr
500	505	510
Lys Leu Arg Ala Gln Gln	Cys Arg Phe Trp Thr	Ser Phe Phe Pro Lys
515	520	525
Val Leu Glu Met Thr Gly	Asn Ile Asp Glu Ala	Glu Trp Glu Trp Lys
530	535	540
Ala Gly Phe His Arg Trp	Asn Asn Tyr Met Met	Asp Trp Lys Asn Gln
545	550	555
Phe Asn Asp Tyr Thr Ser	Lys Lys Glu Ser Cys	Val Gly Leu
565	570	

&lt;210&gt; 179

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

## &lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 179

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc ttt gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe Phe Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	

210	215	220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act aat ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Asn Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
gtt aat aaa gat gaa ggg aca gct ttt tta gcg tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Ala Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Thr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 180

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic Butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 180

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe Phe Gly Ser Glu  
 65 70 75 80



Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
				165					170					175		
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
	210					215					220					
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225				230						235					240	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Asn	Leu	Ser	Val	
		275					280					285				
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Ala	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395					400	
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	
		420						425					430			
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
	450					455					460					
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490					495		
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
		500						505					510			
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	

530		535		540	
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln					
545		550		555	560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu					
	565		570		

<210> 181  
 <211> 1722  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 181

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc ttt gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe Phe Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	

gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggg tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act aat ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Asn Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gcg tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Ala Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152

tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc 1200  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400

cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc 1248  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415

ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa 1296  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430

tgg ctg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta 1344  
 Trp Leu Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 182

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 182

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
1				5					10					15	
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	Phe	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100						105				110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120						125		
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180						185					190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200						205		
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
		210				215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230						235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Asn	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Ala	Tyr	Gly	Ala	Pro	Gly
			325						330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
				405					410					415	

Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Leu Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 183

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 183

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc ttt gga tca gag 240  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe Phe Gly Ser Glu  
 65 70 75 80

atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat 288  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt	672
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser	
210 215 220	
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg	720
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg	
225 230 235 240	
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat	768
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn	
245 250 255	
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att	816
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile	
260 265 270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act aat ttg tca gta	864
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Asn Leu Ser Val	
275 280 285	
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac	912
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp	
290 295 300	
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt	960
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly	
305 310 315 320	
ggt aat aaa gat gaa ggg aca gct ttt tta gcg tat ggt gct cct ggc	1008

Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Ala	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
atc	ctt	ttt	cat	tac	aca	gac	tgg	gtg	gat	gat	cag	aga	cct	gaa	aac	1152
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390				395						400	
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	
				405					410					415		
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	cgg	tgg	cca	gaa	1296
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Arg	Trp	Pro	Glu	
			420					425					430			
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435					440					445				
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	
		450				455					460					
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490					495		
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	
			500					505					510			
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	
		515					520					525				
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	
		530				535					540					
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa	1680
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	



545

550

555

560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

1722

&lt;210&gt; 184

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 184

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe Phe Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Asn Leu Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp

290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Ala Tyr Gly Ala Pro Gly  
 325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350  
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Arg Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 185

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 185

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144

Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser		
		35					40					45					
ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser		
	50					55			60								
tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	ttt	gga	tca	gag	240	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	Phe	Gly	Ser	Glu		
	65				70				75						80		
atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288	
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn		
				85					90						95		
gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp		
			100					105					110				
att	tat	ggg	ggg	ggg	ttt	caa	tgg	gga	aca	tca	tct	tta	cat	gtt	tat	384	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Trp	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		
		115					120					125					
gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met		
	130					135					140						
aac	tat	agg	gtg	ggg	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro		
	145				150				155						160		
gag	gct	cca	ggg	aac	atg	ggg	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln		
				165					170					175			
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggg	gga	aat	cct	aaa	agt	gta	576	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val		
			180					185					190				
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195					200					205					
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
		210					215				220						
ggg	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
	225				230					235					240		
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggg	tgc	tct	aga	gag	aat	768	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		
				245					250					255			
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		

260	265	270	
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act aat ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Asn Leu Ser Val 275 280 285			864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300			912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320			960
ggt aat aaa gat gaa ggg aca gct ttt tta gcg tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Ala Tyr Gly Ala Pro Gly 325 330 335			1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350			1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365			1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380			1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400			1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415			1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430			1296
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445			1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460			1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480			1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495			1488

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 186

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 186

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe Phe Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Trp Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175

Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
		210				215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225					230					235					240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Asn	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
		290				295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Ala	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
		370				375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
				405					410					415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
			420					425					430		
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
		435				440						445			
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser
		450				455					460				
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro
465					470					475					480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr
				485					490					495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr
			500					505					510		
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
		515					520					525			
Val	Leu	Glu													

<210> 187

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 187

gaa	gat	gac	atc	ata	att	gca	aca	aag	aat	gga	aaa	gtc	aga	ggg	atg	48
Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	
1				5					10					15		

aac	ttg	aca	gtt	ttt	ggg	ggc	acg	gta	aca	gcc	ttt	ctt	gga	att	ccc	96
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	
			20					25					30			

tat	gca	cag	cca	cct	ctt	ggg	aga	ctt	cga	ttc	aaa	aag	cca	cag	tct	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	
		35					40					45				

ctg	acc	aag	tgg	tct	gat	att	tgg	aat	gcc	aca	aaa	tat	gca	aat	tct	192
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50					55					60					

tgc	tgt	cag	aac	ata	gat	caa	agt	ttt	cca	ggc	ttc	ttt	gga	tca	gag	240
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	Phe	Gly	Ser	Glu	
65					70					75					80	

atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		

gta	tgg	att	cca	gca	cct	aaa	cca	aaa	aat	gcc	act	gta	ttg	ata	tgg	336
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100					105					110			

att	tat	ggg	ggg	ggg	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115					120					125				

gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					

aac	tat	agg	gtg	ggg	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	

gag	gct	cca	ggg	aac	atg	ggg	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
			165						170					175		

tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggg	gga	aat	cct	aaa	agt	gta	576
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			

act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				

ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggc tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act aat ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Asn Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gcg tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Ala Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggc tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296



tgg atg gga gtg atg cat ggc cag gaa att gaa ttt gtc ttt ggt tta 1344  
 Trp Met Gly Val Met His Gly Gln Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 188

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 188

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser

50		55		60
Cys 65	Cys Gln Asn Ile Asp 70	Gln Ser Phe Pro Gly 75	Phe Phe Gly Ser Glu 80	
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85				
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 90				
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 95				
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 100				
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 105				
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 110				
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 115				
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 120				
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 125				
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 130				
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 135				
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 140				
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Asn Leu Ser Val 145				
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 150				
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 155				
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Ala Tyr Gly Ala Pro Gly 160				
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 165				
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 170				
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 175				
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 180				
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 185				
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 190				
Trp Met Gly Val Met His Gly Gln Glu Ile Glu Phe Val Phe Gly Leu 195				
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 200				
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 205				
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 210				
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr 215				

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<210> 189
<211> 1722
<212> DNA
<213> Artificial Sequence
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<220>
<221> CDS
<222> (1)...(1722)
.
<223> synthetic butyrylcholinesterase variant
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<400> 189																	
gaa	gat	gac	atc	ata	att	gca	aca	aag	aat	gga	aaa	gtc	aga	ggg	atg	48	
Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met		
1			5			10			15								
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc																	96
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro		
			20			25			30								
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct																	144
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser		
35						40			45								
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct																	192
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser		
50						55			60								
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag																	240
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu		
65			70						75			80					
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat																	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn		
			85						90			95					
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg																	336
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp		
			100			105						110					
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat																	384
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		
115						120						125					
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg																	432
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met		
130			135						140								

aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160	480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175	528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190	576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205	624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggg tcc ttt aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Phe Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gtc ttt gtt gtc ccc tat ggg act ccg ttg tca gta Leu Leu Asn Glu Val Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104

atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac	1152
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn	
370 375 380	
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat att ata tgc	1200
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Ile Ile Cys	
385 390 395 400	
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc	1248
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala	
405 410 415	
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa	1296
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu	
420 425 430	
tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta	1344
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu	
435 440 445	
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt	1392
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser	
450 455 460	
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca	1440
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro	
465 470 475 480	
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act	1488
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr	
485 490 495	
gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg	1536
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr	
500 505 510	
aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa	1584
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys	
515 520 525	
gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa	1632
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys	
530 535 540	
gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa	1680
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln	
545 550 555 560	
ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc	1722
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu	
565 570	

&lt;210&gt; 190

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 190

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175  
 Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val  
 180 185 190  
 Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu  
 195 200 205  
 Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser  
 210 215 220  
 Gly Ser Phe Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg  
 225 230 235 240  
 Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn  
 245 250 255  
 Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile  
 260 265 270  
 Leu Leu Asn Glu Val Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val  
 275 280 285  
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp  
 290 295 300  
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly  
 325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350  
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Ile Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu

Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
		435					440					445			
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser
	450					455					460				
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro
465					470					475					480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr
				485					490					495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr
			500					505					510		
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
		515					520					525			
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys
	530					535					540				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln
545					550					555					560
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu		
				565					570						

<210> 191

<211>. 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (1722)$ 

<223> synthetic butyrylcholinesterase variant

<400> 191

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Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
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aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
35 40 45

ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct 192  
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
50 55 60

tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag 240  
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
65 70 75 80

atg	tgg	aac	cca	aac	act	gac	ctc	agt	gaa	gac	tgt	tta	tat	cta	aat	288
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		

gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg 336

Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp		
			100					105					110				
att	tat	ggg	ggg	ggg	ttt	caa	act	gga	aca	tca	tct	tta	cat	gtt	tat	384	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr		
		115					120					125					
gat	ggc	aag	ttt	ctg	gct	cgg	gtt	gaa	aga	gtt	att	gta	gtg	tca	atg	432	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met		
	130					135					140						
aac	tat	agg	gtg	ggg	gcc	cta	gga	ttc	tta	gct	ttg	cca	gga	aat	cct	480	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro		
145					150					155					160		
gag	gct	cga	ggg	aac	atg	ggg	tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	528	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln		
			165						170					175			
tgg	gtt	caa	aaa	aat	ata	gca	gcc	ttt	ggg	gga	aat	cct	aaa	agt	gta	576	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val		
		180						185					190				
act	ctc	ttt	gga	gaa	agt	gca	gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	624	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195					200					205					
ctt	tct	cct	gga	agc	cat	tca	ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	672	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
	210					215					220						
ggg	tcc	gck	aat	gct	cct	tgg	gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	720	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
225					230					235					240		
aac	aga	acg	ttg	aac	tta	gct	aaa	ttg	act	ggg	tgc	tct	aga	gag	aat	768	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		
			245						250					255			
gag	act	gaa	ata	atc	aag	tgt	ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	816	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260					265					270				
ctt	ctg	aat	gaa	gca	ttt	gtt	gtc	ccc	tat	ggg	act	cct	ggg	tca	gta	864	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Gly	Ser	Val		
		275					280					285					
aac	ttt	ggg	ccg	acc	gtg	gat	ggg	gat	ttt	ctc	act	gac	atg	cca	gac	912	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp		
	290					295					300						
ata	tta	ctt	gaa	ctt	gga	caa	ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggg	960	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly		
305					310					315					320		
gtt	aat	aaa	gat	gaa	ggg	aca	gct	ttt	tta	gtc	tcg	ggg	gct	cct	ggc	1008	
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Ser	Gly	Ala	Pro	Gly		



325										330					335					
ttc	agc	aaa	gat	aac	aat	agt	atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	1056				
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu					
			340					345					350							
ggt	tta	aaa	ata	ttt	ttt	cca	gga	gtg	agt	gag	ttt	gga	aag	gaa	tcc	1104				
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser					
		355					360					365								
atc	ctt	ttt	cat	tac	aca	gac	tgg	gta	gat	gat	cag	aga	cct	gaa	aac	1152				
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn					
	370					375					380									
tac	cgt	gag	gcc	ttg	ggt	gat	gtt	gtt	ggg	gat	tat	aat	ttc	ata	tgc	1200				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys					
385					390					395					400					
cct	gcc	ttg	gag	ttc	acc	aag	aag	ttc	tca	gaa	tgg	gga	aat	aat	gcc	1248				
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala					
				405					410					415						
ttt	ttc	tac	tat	ttt	gaa	cac	cga	tcc	tcc	aaa	ctt	ccg	tgg	cca	gaa	1296				
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu					
			420					425					430							
tgg	atg	gga	gtg	atg	cat	ggc	tat	gaa	att	gaa	ttt	gtc	ttt	ggt	tta	1344				
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu					
		435					440					445								
cct	ctg	gaa	aga	aga	gat	aat	tac	aca	aaa	gcc	gag	gaa	att	ttg	agt	1392				
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser					
	450					455					460									
aga	tcc	ata	gtg	aaa	cgg	tgg	gca	aat	ttt	gca	aaa	tat	ggg	aat	cca	1440				
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro					
465					470					475					480					
aat	gag	act	cag	aac	aat	agc	aca	agc	tgg	cct	gtc	ttc	aaa	agc	act	1488				
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr					
				485					490					495						
gaa	caa	aaa	tat	cta	acc	ttg	aat	aca	gag	tca	aca	aga	ata	atg	acg	1536				
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr					
			500					505					510							
aaa	cta	cgt	gct	caa	caa	tgt	cga	ttc	tgg	aca	tca	ttt	ttt	cca	aaa	1584				
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys					
		515					520					525								
gtc	ttg	gaa	atg	aca	gga	aat	att	gat	gaa	gca	gaa	tgg	gag	tgg	aaa	1632				
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys					
	530					535					540									
gca	gga	ttc	cat	cgc	tgg	aac	aat	tac	atg	atg	gac	tgg	aaa	aat	caa	1680				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln					
545					550						555				560					

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

1722

&lt;210&gt; 192

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;220&gt;

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 192

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met
1				5					10					15	
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
			35				40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75				80	
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
		115					120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155				160	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225					230					235				240	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
			260					265					270		
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Gly	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				

Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly  
 305 310 315 320  
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Ser Gly Ala Pro Gly  
 325 330 335  
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu  
 340 345 350  
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser  
 355 360 365  
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn  
 370 375 380  
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys  
 385 390 395 400  
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala  
 405 410 415  
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu  
 420 425 430  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
 435 440 445  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
 450 455 460  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
 465 470 475 480  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
 485 490 495  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 193

<211> 1722

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1722)

<223> synthetic butyrylcholinesterase variant

<400> 193

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg 48  
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15

aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc 96  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30

tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct 144  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser

35	40	45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser 50 55 60			192
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu 65 70 75 80			240
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn 85 90 95			288
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp 100 105 110			336
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr 115 120 125			384
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met 130 135 140			432
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro 145 150 155 160			480
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln 165 170 175			528
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val 180 185 190			576
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu 195 200 205			624
ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220			672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240			720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255			768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270			816

ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gtc tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggg tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ctc tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Leu Trp Pro Glu 420 425 430	1296
tgg gtt gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta Trp Val Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu 435 440 445	1344
cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser 450 455 460	1392
aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro 465 470 475 480	1440
aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr 485 490 495	1488

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
 500 505 510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
 515 520 525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
 530 535 540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
 545 550 555 560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
 565 570

<210> 194

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 194

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1 5 10 15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
 20 25 30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
 35 40 45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser  
 50 55 60  
 Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu  
 65 70 75 80  
 Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn  
 85 90 95  
 Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp  
 100 105 110  
 Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr  
 115 120 125  
 Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met  
 130 135 140  
 Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro  
 145 150 155 160  
 Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln  
 165 170 175

Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val		
			180					185					190				
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu		
		195					200					205					
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser		
	210					215					220						
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg		
225					230					235					240		
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn		
				245					250					255			
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile		
			260					265					270				
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val		
		275					280					285					
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp		
	290					295					300						
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly		
305					310					315					320		
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly		
				325					330					335			
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu		
			340					345					350				
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser		
		355					360					365					
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn		
	370					375					380						
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys		
385					390					395					400		
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala		
				405					410					415			
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Leu	Trp	Pro	Glu		
		420						425					430				
Trp	Val	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu		
		435					440					445					
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser		
	450					455					460						
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro		
465					470					475					480		
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr		
				485					490					495			
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr		
			500					505					510				
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys		
		515					520					525					
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys		
	530					535					540						
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln		
545					550					555					560		
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu				
				565					570								

&lt;210&gt; 195

&lt;211&gt; 1722

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1722)

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;400&gt; 195

gaa gat gac atc ata att gca aca aag aat gga aaa gtc aga ggg atg	48
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met	
1 5 10 15	
aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc	96
Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro	
20 25 30	
tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag cca cag tct	144
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser	
35 40 45	
ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat gca aat tct	192
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser	
50 55 60	
tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat gga tca gag	240
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu	
65 70 75 80	
atg tgg aac cca aac act gac ctc agt gaa gac tgt tta tat cta aat	288
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn	
85 90 95	
gta tgg att cca gca cct aaa cca aaa aat gcc act gta ttg ata tgg	336
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp	
100 105 110	
att tat ggt ggt ggt ttt caa act gga aca tca tct tta cat gtt tat	384
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr	
115 120 125	
gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta gtg tca atg	432
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met	
130 135 140	
aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca gga aat cct	480
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro	
145 150 155 160	
gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg gct ctt cag	528
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln	
165 170 175	
tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct aaa agt gta	576
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val	
180 185 190	
act ctc ttt gga gaa agt gca gga gca gct tca gtt agc ctg cat ttg	624
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu	
195 200 205	



ctt tct cct gga agc cat tca ttg ttc acc aga gcc att ctg caa agt Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser 210 215 220	672
ggt tcc gck aat gct cct tgg gcg gta aca tct ctt tat gaa gct agg Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg 225 230 235 240	720
aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct aga gag aat Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn 245 250 255	768
gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc caa gaa att Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile 260 265 270	816
ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act aat ttg tca gta Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Asn Leu Ser Val 275 280 285	864
aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac atg cca gac Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp 290 295 300	912
ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly 305 310 315 320	960
gtt aat aaa gat gaa ggg aca gct ttt tta gcg tat ggt gct cct ggc Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Ala Tyr Gly Ala Pro Gly 325 330 335	1008
ttc agc aaa gat aac aat agt atc ata act aga aaa gaa ttt cag gaa Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu 340 345 350	1056
ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser 355 360 365	1104
atc ctt ttt cat tac aca gac tgg gta gat gat cag aga cct gaa aac Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn 370 375 380	1152
tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys 385 390 395 400	1200
cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga aat aat gcc Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala 405 410 415	1248
ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu 420 425 430	1296

tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta 1344  
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu  
           435                          440                          445

cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa att ttg agt 1392  
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser  
           450                          455                          460

aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca 1440  
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro  
           465                          470                          475                          480

aat gag act cag aac aat agc aca agc tgg cct gtc ttc aaa agc act 1488  
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr  
                                   485                          490                          495

gaa caa aaa tat cta acc ttg aat aca gag tca aca aga ata atg acg 1536  
 Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr  
                                   500                          505                          510

aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa 1584  
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys  
                                   515                          520                          525

gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg gag tgg aaa 1632  
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys  
           530                          535                          540

gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg aaa aat caa 1680  
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln  
           545                          550                          555                          560

ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt ctc 1722  
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu  
                                   565                          570

<210> 196

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

<221>VARIANT

<222> 227

<223> Xaa = Ala

<400> 196

Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met  
 1                          5                          10                          15  
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro  
                           20                          25                          30  
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser  
                           35                          40                          45  
 Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser

50	55	60
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu		
65	70	75
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn		80
	85	90
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp		95
	100	105
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr		110
	115	120
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met		125
	130	135
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro		140
	145	150
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln		155
	160	165
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val		170
	175	180
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu		185
	190	195
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser		200
	205	210
Gly Ser Xaa Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg		215
	220	225
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn		230
	235	240
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile		245
	250	255
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Asn Leu Ser Val		260
	265	270
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp		275
	280	285
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly		290
	295	300
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Ala Tyr Gly Ala Pro Gly		305
	310	315
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu		320
	325	330
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser		335
	340	345
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn		350
	355	360
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys		365
	370	375
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala		380
	385	390
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu		395
	400	405
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu		410
	415	420
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser		425
	430	435
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro		440
	445	450
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr		455
	460	465
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr		470
	475	480
	485	490
	495	500
	505	510

Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
		515					520					525			
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys
	530					535					540				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln
545					550					555					560
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu		
				565					570						

<210> 197

<211> 642

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> synthetic butyrylcholinesterase variant

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (642)$ 

<400> 197

gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg 48  
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agc tca agt gta ccg tac atc 96  
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Pro Tyr Ile  
20 25 30

cac tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc atc tat      144  
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr  
              35                     40                     45

```
gcc aca tcc gct ctg gct tct ggc atc cca gac agg ttc agt ggc agt      192
Ala Thr Ser Ala Leu Ala Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
      50                      55                      60
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ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag cct gaa 240  
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu  
65 70 75 80

gat ttt gca gtg tat tac tgt cag cag tgg ctg agt aac cca ccc act 288  
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Leu Ser Asn Pro Pro Thr  
85 90 95

ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg gct gca cca 336  
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro  
100 105 110

tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act 384  
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
115 120 125

gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa 432  
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
130 135 140

gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag 480  
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
 145 150 155 160

agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc agc 528  
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser  
 165 170 175

acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc 576  
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
 180 185 190

tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc 624  
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
 195 200 205

aac agg gga gag tgt tag 642  
 Asn Arg Gly Glu Cys \*  
 210

<210> 198

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<400> 198

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Pro Tyr Ile  
 20 25 30  
 His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr  
 35 40 45  
 Ala Thr Ser Ala Leu Ala Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser  
 50 55 60  
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu  
 65 70 75 80  
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Leu Ser Asn Pro Pro Thr  
 85 90 95  
 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro  
 100 105 110  
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
 115 120 125  
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
 130 135 140  
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
 145 150 155 160  
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser  
 165 170 175  
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
 180 185 190  
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
 195 200 205  
 Asn Arg Gly Glu Cys  
 210

&lt;210&gt; 199

<400> 199  
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&lt;210&gt; 200

<400> 200  
000

&lt;210&gt; 201

&lt;211&gt; 2298

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic butyrylcholinesterase variant

&lt;221&gt; CDS

&lt;222&gt; (1)...(2298)

&lt;400&gt; 201

gag	gtg	cag	ctg	gtg	cag	tct	gga	gca	gag	gtg	aaa	aag	ccc	ggg	gag	48
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu	
1				5					10					15		

tct	ctg	aag	atc	tcc	tgt	aag	ggt	tct	ggc	cgt	aca	ttt	acc	agt	tac	96
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Arg	Thr	Phe	Thr	Ser	Tyr	
			20					25					30			

aat	atg	cac	tgg	gtg	cgc	cag	atg	ccc	ggg	aaa	ggc	ctg	gag	tgg	atg	144
Asn	Met	His	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met	
		35					40					45				

ggg	gct	att	tat	ccc	ttg	acg	ggt	gat	act	tcc	tac	aat	cag	aag	tcg	192
Gly	Ala	Ile	Tyr	Pro	Leu	Thr	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Ser	
	50					55					60					

aaa	ctc	cag	gtc	acc	atc	tca	gcc	gac	aag	tcc	atc	agc	acc	gcc	tac	240
Lys	Leu	Gln	Val	Thr	Ile	Ser	Ala	Asp	Lys	Ser	Ile	Ser	Thr	Ala	Tyr	
	65				70				75					80		

ctg	cag	tgg	agc	agc	ctg	aag	gcc	tcg	gac	acc	gcc	atg	tat	tac	tgt	288
Leu	Gln	Trp	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	
				85					90					95		

gcg	aga	tcg	act	tac	gtg	ggc	ggt	gac	tgg	cag	ttc	gat	gtc	tgg	ggc	336
Ala	Arg	Ser	Thr	Tyr	Val	Gly	Gly	Asp	Trp	Gln	Phe	Asp	Val	Trp	Gly	
			100					105					110			

aag	ggg	acc	acg	gtc	acc	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	384
Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
		115					120					125				

gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	432
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	

130	135	140	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 145 150 155 160			480
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 165 170 175			528
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 180 185 190			576
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 195 200 205			624
aag ccc agc aac acc aag gtg gac aag aaa gca gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser Cys 210 215 220			672
gac aaa act cac aca tgc cca ccg tgc cca aag ctt gaa gat gac atc Asp Lys Thr His Thr Cys Pro Pro Cys Pro Lys Leu Glu Asp Asp Ile 225 230 235 240			720
ata att gca aca aag aat gga aaa gtc aga ggg atg aac ttg aca gtt Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met Asn Leu Thr Val 245 250 255			768
ttt ggt ggc acg gta aca gcc ttt ctt gga att ccc tat gca cag cca Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro Tyr Ala Gln Pro 260 265 270			816
cct ctt ggt aga ctt cga ttc aaa aag cca cag tct ctg acc aag tgg Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys Trp 275 280 285			864
tct gat att tgg aat gcc aca aaa tat gca aat tct tgc tgt cag aac Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser Cys Cys Gln Asn 290 295 300			912
ata gat caa agt ttt cca ggc ttc ttt gga tca gag atg tgg aac cca Ile Asp Gln Ser Phe Pro Gly Phe Phe Gly Ser Glu Met Trp Asn Pro 305 310 315 320			960
aac act gac ctc agt gaa gac tgt tta tat cta aat gta tgg att cca Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ile Pro 325 330 335			1008
gca cct aaa cca aaa aat gcc act gta ttg ata tgg att tat ggt ggt Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp Ile Tyr Gly Gly 340 345 350			1056
ggt ttt caa act gga aca tca tct tta cat gtt tat gat ggc aag ttt Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr Asp Gly Lys Phe 355 360 365			1104

ctg gct cgg gtt gaa aga gtt att gta gtg tca atg aac tat agg gtg Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met Asn Tyr Arg Val 370 375 380	1152
ggg gcc cta gga ttc tta gct ttg cca gga aat cct gag gct cca ggg Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro Glu Ala Pro Gly 385 390 395 400	1200
aac atg ggt tta ttt gat caa cag ttg gct ctt cag tgg gtt caa aaa Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln Trp Val Gln Lys 405 410 415	1248
aat ata gca gcc ttt ggt gga aat cct aaa agt gta act ctc ttt gga Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val Thr Leu Phe Gly 420 425 430	1296
gaa agt gca gga gca gct tca gtt agc ctg cat ttg ctt tct cct gga Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu Leu Ser Pro Gly 435 440 445	1344
agc cat tca ttg ttc acc aga gcc att ctg caa agt ggt tcc gct aat Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser Gly Ser Ala Asn 450 455 460	1392
gct cct tgg gcg gta aca tct ctt tat gaa gct agg aac aga acg ttg Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg Asn Arg Thr Leu 465 470 475 480	1440
aac tta gct aaa ttg act ggt tgc tct aga gag aat gag act gaa ata Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn Glu Thr Glu Ile 485 490 495	1488
atc aag tgt ctt aga aat aaa gat ccc caa gaa att ctt ctg aat gaa Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile Leu Leu Asn Glu 500 505 510	1536
gca ttt gtt gtc ccc tat ggg act aat ttg tca gta aac ttt ggt ccg Ala Phe Val Val Pro Tyr Gly Thr Asn Leu Ser Val Asn Phe Gly Pro 515 520 525	1584
acc gtg gat ggt gat ttt ctc act gac atg cca gac ata tta ctt gaa Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp Ile Leu Leu Glu 530 535 540	1632
ctt gga caa ttt aaa aaa acc cag att ttg gtg ggt gtt aat aaa gat Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly Val Asn Lys Asp 545 550 555 560	1680
gaa ggg aca gct ttt tta gcg tat ggt gct cct ggc ttc agc aaa gat Glu Gly Thr Ala Phe Leu Ala Tyr Gly Ala Pro Gly Phe Ser Lys Asp 565 570 575	1728
aac aat agt atc ata act aga aaa gaa ttt cag gaa ggt tta aaa ata Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu Gly Leu Lys Ile 580 585 590	1776



ttt ttt cca gga gtg agt gag ttt gga aag gaa tcc atc ctt ttt cat 1824  
 Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser Ile Leu Phe His  
 595 600 605  
  
 tac aca gac tgg gta gat gat cag aga cct gaa aac tac cgt gag gcc 1872  
 Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr Arg Glu Ala  
 610 615 620  
  
 ttg ggt gat gtt gtt ggg gat tat aat ttc ata tgc cct gcc ttg gag 1920  
 Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys Pro Ala Leu Glu  
 625 630 635 640  
  
 ttc acc aag aag ttc tca gaa tgg gga aat aat gcc ttt ttc tac tat 1968  
 Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr Tyr  
 645 650 655  
  
 ttt gaa cac cga tcc tcc aaa ctt ccg tgg cca gaa tgg atg gga gtg 2016  
 Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met Gly Val  
 660 665 670  
  
 atg cat ggc tat gaa att gaa ttt gtc ttt ggt tta cct ctg gaa aga 2064  
 Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu Glu Arg  
 675 680 685  
  
 aga gat aat tac aca aaa gcc gag gaa att ttg agt aga tcc ata gtg 2112  
 Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile Val  
 690 695 700  
  
 aaa cgg tgg gca aat ttt gca aaa tat ggg aat cca aat gag act cag 2160  
 Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn Glu Thr Gln  
 705 710 715 720  
  
 aac aat agc aca agc tgg cct gtc ttc aaa agc act gaa caa aaa tat 2208  
 Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys Tyr  
 725 730 735  
  
 cta acc ttg aat aca gag tca aca aga ata atg acg aaa cta cgt gct 2256  
 Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr Lys Leu Arg Ala  
 740 745 750  
  
 caa caa tgt cga ttc tgg aca tca ttt ttt cca aaa gtc tga 2298  
 Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys Val \*  
 755 760 765

&lt;210&gt; 202

&lt;211&gt; 765

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic btyrylcholinesterase variant

&lt;400&gt; 202

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15  
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Arg Thr Phe Thr Ser Tyr  
 20 25 30

Asn	Met	His	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Ala	Ile	Tyr	Pro	Leu	Thr	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Ser
	50					55					60				
Lys	Leu	Gln	Val	Thr	Ile	Ser	Ala	Asp	Lys	Ser	Ile	Ser	Thr	Ala	Tyr
65					70					75					80
Leu	Gln	Trp	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Ser	Thr	Tyr	Val	Gly	Gly	Asp	Trp	Gln	Phe	Asp	Val	Trp	Gly
			100					105					110		
Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
		115					120					125			
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
	130					135					140				
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
145					150					155					160
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
				165					170					175	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
			180					185					190		
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
		195					200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys
	210					215					220				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Lys	Leu	Glu	Asp	Asp	Ile
225					230					235					240
Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	Asn	Leu	Thr	Val
				245					250					255	
Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	Tyr	Ala	Gln	Pro
			260					265					270		
Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	Leu	Thr	Lys	Trp
		275					280					285			
Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	Cys	Cys	Gln	Asn
	290					295					300				
Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	Phe	Gly	Ser	Glu	Met	Trp	Asn	Pro
305					310					315					320
Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ile	Pro
				325					330					335	
Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	Ile	Tyr	Gly	Gly
			340					345					350		
Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	Asp	Gly	Lys	Phe
		355					360					365			
Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	Asn	Tyr	Arg	Val
	370					375					380				
Gly	Ala	Leu	Gly	Phe	Leu										

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<210> 203
<220>
<223> synthetic butyrylcholinesterase variant
<400> 203
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<210> 204
<211> 530
<212> PRT
<213> Artificial Sequence
<220>
<223> synthetic butyrylcholinesterase variant
<220>
<221>VARIANT
<222> 227

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<220>

<223> synthetic butyrylcholinesterase variant

<400> 203

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<210> 204

<211> 530

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic butyrylcholinesterase variant

<220>

&lt;221&gt;VARIANT

&lt;222&gt; 227

&lt;223&gt; Xaa = Ala

&lt;400&gt; 204

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	Phe	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Xaa	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Asn	Leu	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Ala	Tyr	Gly	Ala	Pro	Gly	325	330	335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350	
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365	
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380	
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395	400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430	

[illegible]